

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:21 ; Search time 6503.04 Seconds
(without alignments)
10141.035 Million cell updates/sec

Title: US-09-922-067F-9
Perfect score: 1361
Sequence: 1 tgagagactaagctgaaact.....aggaatagagaatacaatt 1361

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues 9416466
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	GenEmbl:*
1:	gb_ba:*
2:	gb_hcg:*
3:	gb_in:*
4:	gb_om:*
5:	gb_ov:*
6:	gb_pat:*
7:	gb_ph:*
8:	gb_pl:*
9:	gb_pr:*
10:	gb_ro:*
11:	gb_sts:*
12:	gb_sy:*
13:	gb_un:*
14:	gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1361	100.0	1361	6 A41956	A41956 Sequence 9
2	1361	100.0	1361	6 AR080658	AR080658 Sequence
3	1361	100.0	1361	6 AR084987	AR084987 Sequence
4	1361	100.0	1361	6 AR125358	AR125358 Sequence
5	1361	100.0	1361	6 BD242703	BD242703 Method fo
6	1361	100.0	1361	6 AR205614	AR205614 Sequence
7	1361	100.0	1361	6 AX006795	AX006795 Sequence
8	1361	100.0	1561	6 AX335487	AX335487 Sequence
9	1361	100.0	1561	9 HSU24577	U24577 Human LDL-p
10	1359.4	99.9	1505	6 CQ717247	CQ717247 Sequence
11	1359.4	99.9	1505	9 HSU20157	U20157 Human plate
12	1359.4	99.9	1520	6 A81377	A81377 Sequence 7
13	1359.4	99.9	1520	6 AR064404	AR064404 Sequence
14	1359.4	99.9	1520	6 AR083755	AR083755 Sequence
15	1359.4	99.9	1520	6 AR141150	AR141150 Sequence
16	1359.4	99.9	1520	6 AR142503	AR142503 Sequence
17	1359.4	99.9	1520	6 I23385	I23385 Sequence 7
18	1359.4	99.9	1520	6 I49901	I49901 Sequence 7
19	1359.4	99.9	1520	6 I60362	I60362 Sequence 7

20	1359.4	99.9	1520	6 I85595	I85595 Sequence 7
21	1358	99.8	1554	9 BC038452	BC038452 Homo sapi
22	1162.4	85.4	1335	6 A81400	A81400 Sequence 30
23	1162.4	85.4	1335	6 AR064425	AR064425 Sequence
24	1162.4	85.4	1335	6 AR083776	AR083776 Sequence
25	1162.4	85.4	1335	6 AR141171	AR141171 Sequence
26	1162.4	85.4	1335	6 AR142524	AR142524 Sequence
27	1162.4	85.4	1335	6 I60383	I60383 Sequence 30
28	1049.6	77.1	1506	4 BTU34247	U34247 Bovine plas
29	1049.6	77.1	1533	6 A81393	A81393 Sequence 23
30	1049.6	77.1	1533	6 AR064419	AR064419 Sequence
31	1049.6	77.1	1533	6 AR083770	AR083770 Sequence
32	1049.6	77.1	1533	6 AR141165	AR141165 Sequence
33	1049.6	77.1	1533	6 AR142518	AR142518 Sequence
34	1049.6	77.1	1533	6 I60377	I60377 Sequence 23
35	1043.2	76.6	2191	6 A81392	A81392 Sequence 22
36	1043.2	76.6	2191	6 AR064418	AR064418 Sequence
37	1043.2	76.6	2191	6 AR083769	AR083769 Sequence
38	1043.2	76.6	2191	6 AR141164	AR141164 Sequence
39	1043.2	76.6	2191	6 AR142517	AR142517 Sequence
40	1043.2	76.6	2191	6 I49915	I49915 Sequence 22
41	1043.2	76.6	2191	6 I60376	I60376 Sequence 22
42	1043.2	76.6	2191	6 I85609	I85609 Sequence 22
43	1043.2	76.6	2222	4 CFU34246	U34246 Dog plasma
44	808.2	59.4	1669	10 BC010726	BC010726 Mus muscu
45	796.8	58.5	2909	10 D67037	D67037 Guinea pig

ALIGNMENTS

RESULT 1

A41956

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CDS

Sequence 9 from Patent WO9500649.
A41956
A41956
A41956.1 GI:2297493
unidentified
unidentified
unclassified.
1 (bases 1 to 1361)
Macphee,C.H., Tew,D.G., Southan,C.D., Hickey,D.M., Gloger,I.S.,
Lawrence,G.M. and Rice,S.Q.
LIPOPROTEIN ASSOCIATED PHOSPHOLIPASE A 2?, INHIBITORS THEREOF AND
USE OF THE SAME IN DIAGNOSIS AND THERAPY
Patent: WO 9500649-A 9 05-JAN-1995;
SMITHKLINE BEECHAM PLC (GB)
Other publication JP 8500740T 960130.
Location/Qualifiers
1. .1361
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
38. .>1361
/note="unnamed protein product"
/codon_start=1
/protein_id="CAA02638.1"
/db_xref="GI:2297494"
/translation="MVPPKLVHLCGCLAVVYPPDWQYINPVAHMKSSAWVNKIQV
LMAASFQGTIKIPRGNGPYSVCGTDLMDHTNKGTFRLLYYPSQDNDRDLTLWIPNKE
YFWGLSKPLGTHWLMGNILRLFGSMTPANWNSPLRPGEKYPLVVFSGHGLGAFRTLY
SAIGIDLASHGFTVAVEHRDRSASATYFKDQSAAEIGDKSWLYRLTKQEEETHIR
NEQVRORAKESQALSILIDIDHGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSFGG
ATVIQLSEDRFCRGIALDAWMFPLGDEVYSRIPQPLFFINSEYFQYFANIIMKKKC
YSPDKERKMITIRGVSQNFADFTFATGKIIGHMLKLGKGDIDSNAAIDLSNKASLAFL
QKHLGLHKDFDQWDCLEGGDDENLIPGTNINTTQNHMLQNSSGIEKYN"

ORIGIN

Query Match 100.0%; Score 1361; DB 6; Length 1361;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTGCATGT 60
Db 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTGCATGT 60
QY 61 GCTTTTCTGCCCTCTGGGGCTGCCTGGCTGTGGTTATCCTTTTGACTGGCAATACATAAA 120
Db 61 GCTTTTCTGCCCTCTGGGGCTGCCTGGCTGTGGTTATCCTTTTGACTGGCAATACATAAA 120
QY 121 TCCTGTTGCCCATATGAAANTCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
Db 121 TCCTGTTGCCCATATGAAANTCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCGGTTGGTTGTAC 240
Db 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCGGTTGGTTGTAC 240
QY 241 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTCTTGGCTTTATATATCCATCCCA 300
Db 241 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTCTTGGCTTTATATATCCATCCCA 300
QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGTCCTTAG 360
Db 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGTCCTTAG 360
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
QY 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCTGGTGAAATAATCCACTTGTGT 480
Db 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCTGGTGAAATAATCCACTTGTGT 480
QY 481 TTTTCTCATGCTTGGGCACTTGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 540
Db 481 TTTTCTCATGCTTGGGCACTTGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 540
QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
QY 601 CTATTTCAAGGACCAATCTGCTCAGAAATAGGGGACAACTTGGCTCTACTTTAGAAC 660
Db 601 CTATTTCAAGGACCAATCTGCTCAGAAATAGGGGACAACTTGGCTCTACTTTAGAAC 660
QY 661 CCTGAAACAAGAGGAGGAGACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 661 CCTGAAACAAGAGGAGGAGACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
Db 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840
Db 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840
QY 841 AGTAATTGGACATTTCTTTTGGTGAGCAACGCTTATTCAGACTCTTAGTGAAGATCAGAG 900
Db 841 AGTAATTGGACATTTCTTTTGGTGAGCAACGCTTATTCAGACTCTTAGTGAAGATCAGAG 900
QY 901 ATTACAGATGTGATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 901 ATTACAGATGTGATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
QY 961 CAGAAATCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATAT 1020
Db 961 CAGAAATCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATAT 1020
QY 1021 CATAAAAATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db 1021 CATAAAAATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAATCAGGGG 1080
QY 1081 TTCAGTCCACAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140

Db 1081 TTCAAGTCCACCAAGAAATTTTGTGCTGACTTTCATTTTGCAACTGGCAAAATAATTGGACACAT 1140
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGAGCTATTGATCTTAGCAACAAGCTTC 1200
Db 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGAGCTATTGATCTTAGCAACAAGCTTC 1200
QY 1201 ATTAGCATTTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGTAGTGGGACTGCTT 1260
Db 1201 ATTAGCATTTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGTAGTGGGACTGCTT 1260
QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGACCAACATTAACACCAATCAACA 1320
Db 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGACCAACATTAACACCAATCAACA 1320
QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361
Db 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361
RESULT 2
LOCUS AR080658 1361 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 9 from patent US 5968818.
ACCESSION AR080658
VERSION AR080658.1 GI:10007388
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1361)
AUTHORS Gloger, I. Simon., Lawrence, G. Mark, Prouse. and Rice, S. Quentyn. John.
TITLE Lipoprotein associated phospholipase A2, inhibitors thereof and use of the same in diagnosis and therapy
JOURNAL Patent: US 5968818-A 9 19-OCT-1999;
FEATURES
source Location/Qualifiers
1. .1361
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 1361; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTGCATGT 60
Db 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTGCATGT 60
QY 61 GCTTTTCTGCCCTCTGGGGCTGCCTGGCTGTGGTTATCCTTTTGACTGGCAATACATAAA 120
Db 61 GCTTTTCTGCCCTCTGGGGCTGCCTGGCTGTGGTTATCCTTTTGACTGGCAATACATAAA 120
QY 121 TCCTGTTGCCCATATGAAANTCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
Db 121 TCCTGTTGCCCATATGAAANTCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCGGTTGGTTGTAC 240
Db 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCGGTTGGTTGTAC 240
QY 241 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTCTTGGCTTTATATATCCATCCCA 300
Db 241 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTCTTGGCTTTATATATCCATCCCA 300
QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGTCCTTAG 360
Db 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGTCCTTAG 360
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420

```
QY 421 GACAACTCCTGCAAACTGGAATCCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT 480
Db 421 GACAACTCCTGCAAACTGGAATCCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT 480
QY 481 TTTTCTCATGTCCTGGGGCATTCAGGACACTTTATCTGCTATTTGGCATTGACCTGGC 540
Db 481 TTTTCTCATGTCCTGGGGCATTCAGGACACTTTATCTGCTATTTGGCATTGACCTGGC 540
QY 541 ATCTCATGGGTTTATAGTTGCTGCTGAGAACACAGAGATAGATCTGCAACTTA 600
Db 541 ATCTCATGGGTTTATAGTTGCTGCTGAGAACACAGAGATAGATCTGCAACTTA 600
QY 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGCAAGTCTTTGGCTCTACCTTAGAAC 660
Db 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGCAAGTCTTTGGCTCTACCTTAGAAC 660
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGACATGATGAAAGCCAGTGAAGATGC 780
Db 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGACATGATGAAAGCCAGTGAAGATGC 780
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840
Db 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840
QY 841 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGTCAGAG 900
Db 841 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGTCAGAG 900
QY 901 ATTGAGATGTGGTATTTGCCCTGGATGTCATGGATGTTTCCACTGGGTGATGAAGTATTC 960
Db 901 ATTGAGATGTGGTATTTGCCCTGGATGTCATGGATGTTTCCACTGGGTGATGAAGTATTC 960
QY 961 CAGAATTCCTCAGCCCTCTTTTATCAACTCTGATATTTCCATATCTCTGCTAATAT 1020
Db 961 CAGAATTCCTCAGCCCTCTTTTATCAACTCTGATATTTCCATATCTCTGCTAATAT 1020
QY 1021 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db 1021 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
QY 1081 TTCAGTCCACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACAT 1140
Db 1081 TTCAGTCCACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACAT 1140
QY 1141 GCTCAAAATTAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTC 1200
Db 1141 GCTCAAAATTAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTC 1200
QY 1201 ATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAGTGGACTGCTT 1260
Db 1201 ATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAGTGGACTGCTT 1260
QY 1261 GATTGAAGGAGATGATGAGAACTTTATCCAGGGACCAACATTAAACAACCAATCAACA 1320
Db 1261 GATTGAAGGAGATGATGAGAACTTTATCCAGGGACCAACATTAAACAACCAATCAACA 1320
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
```

```
RESULT 3
LOCUS AR084987 1361 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 9 from patent US 5981252.
ACCESSION AR084987
VERSION AR084987.1 GI:10011758
KEYWORDS Unknown.
```

```
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1361)
AUTHORS MacPhee,C.Houston. and Tew,D.Graham.
TITLE Lipoprotein associated phospholipase A.sub.2, inhibitors thereof
JOURNAL Patent: US 5981252-A 9 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..1361
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 1361; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 60
Db 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 60
QY 61 GCTTTTCTGCCCTCTCGGGCTGCCCTGGCTGTGGTTTATCCTTTTGAATGGAATACATAA 120
Db 61 GCTTTTCTGCCCTCTCGGGCTGCCCTGGCTGTGGTTTATCCTTTTGAATGGAATACATAA 120
QY 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAAAATACAAGTACTGATGGTGC 180
Db 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAAAATACAAGTACTGATGGTGC 180
QY 181 TGCAAGCTTTGGCCAAACTAAATFCCCGGGGAAATGGGCCTTATTCGTTGGTTGTATC 240
Db 181 TGCAAGCTTTGGCCAAACTAAATFCCCGGGGAAATGGGCCTTATTCGTTGGTTGTATC 240
QY 241 AGACTTAATGTTTGAATCACACTAATAAGGGCACCTTCTTGCGTTTATATATCCATCCCA 300
Db 241 AGACTTAATGTTTGAATCACACTAATAAGGGCACCTTCTTGCGTTTATATATCCATCCCA 300
QY 301 AGATAATGATCGCTTGACACCCTTTGGATCCCAAAATAAAGAAATATTTTGGGGTCTTAG 360
Db 301 AGATAATGATCGCTTGACACCCTTTGGATCCCAAAATAAAGAAATATTTTGGGGTCTTAG 360
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
QY 421 GACAACTCCTGCAAACTGGAATTCCTCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT 480
Db 421 GACAACTCCTGCAAACTGGAATTCCTCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT 480
QY 481 TTTTCTCATGTCCTTGGGGCATTCAGGACACTTTATCTGCTATTTGGCATTGACCTGGC 540
Db 481 TTTTCTCATGTCCTTGGGGCATTCAGGACACTTTATCTGCTATTTGGCATTGACCTGGC 540
QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCAACTTA 600
Db 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCAACTTA 600
QY 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGCAAGTCTTTGGCTCTACCTTAGAAC 660
Db 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGCAAGTCTTTGGCTCTACCTTAGAAC 660
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGACATGATGAAAGCCAGTGAAGATGC 780
Db 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGACATGATGAAAGCCAGTGAAGATGC 780
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840
Db 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840
```

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1361)
AUTHORS MacPhee,C.Houston. and Tew,D.Graham.
TITLE Lipoprotein associated phospholipase A.sub.2, inhibitors thereof
JOURNAL Patent: US 5981252-A 9 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..1361
/organism="unknown"
/mol_type="unassigned DNA"

```
QY 841 AGTAATTGGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 841 AGTAATTGGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
QY 901 ATTGAGATGTGGTATTCCTTGGATGATGAGTGTTCACCTGGTGTGATGAAGTATATTC 960
Db 901 ATTGAGATGTGGTATTCCTTGGATGATGAGTGTTCACCTGGTGTGATGAAGTATATTC 960
QY 961 CAGAATTCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1020
Db 961 CAGAATTCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1020
QY 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080
Db 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080
QY 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140
Db 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140
QY 1141 GCTCAAAATTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1141 GCTCAAAATTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
QY 1201 ATTAGCATCTTACAAAAGCAATTTAGGACITTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1201 ATTAGCATCTTACAAAAGCAATTTAGGACITTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
QY 1261 GATTGAAGGAGATGATGAGAACTTTATCCAGGACCAACATTAACACCAATCAACA 1320
Db 1261 GATTGAAGGAGATGATGAGAACTTTATCCAGGACCAACATTAACACCAATCAACA 1320
QY 1321 CATCATGTTACAGAACTCTTCCAGGAATAGAGAAATACAATT 1361
Db 1321 CATCATGTTACAGAACTCTTCCAGGAATAGAGAAATACAATT 1361

RESULT 4
ARI25358
LOCUS ARI25358 1361 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6177257.
ACCESSION ARI25358
VERSION ARI25358.1 GI:14111420
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1361)
AUTHORS Macphee,C.Houston., Tew,D.Graham., Southan,C.Donald.,
Hickey,D.Mary.Bernadette., Gloger,I.Simon., Lawrence,G.Mark.Prouse.
and Rice,S.Quentyn.John.
TITLE Lipoprotein associated phospholipase A2, inhibitors thereof and use
of the same in diagnosis and therapy
JOURNAL Patent: US 6177257-A 9 23-JAN-2001;
FEATURES
source Location/Qualifiers
1..1361
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 1361; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCACCAATTCATGT 60
Db 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCACCAATTCATGT 60
QY 61 GCTTTTCTGCTCTGCGGCTGCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATAAA 120
Db 61 GCTTTTCTGCTCTGCGGCTGCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATAAA 120
QY 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGC 180
```

```
Db 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGC 180
QY 181 TGCAAGCTTTGGCCAAACTAAAAATCCCCCGGGGAAATGGGCCTTATTCGGTTGGTTGTAC 240
Db 181 TGCAAGCTTTGGCCAAACTAAAAATCCCCCGGGGAAATGGGCCTTATTCGGTTGGTTGTAC 240
QY 241 AGACTTAATGTTTGTATCACACTAATAAAGGCACCTTCTTGCCTTTATATATCCATCCCA 300
Db 241 AGACTTAATGTTTGTATCACACTAATAAAGGCACCTTCTTGCCTTTATATATCCATCCCA 300
QY 301 AGATAATGATCGCCCTTGACACCCCTTTGGATCCCAAAATAAAGAATAATTTTGGGGTCTTAG 360
Db 301 AGATAATGATCGCCCTTGACACCCCTTTGGATCCCAAAATAAAGAATAATTTTGGGGTCTTAG 360
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
QY 421 GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCCCTGGTGAAAAATATCCACTTGTGT 480
Db 421 GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCCCTGGTGAAAAATATCCACTTGTGT 480
QY 481 TTTTCTCATGGTCTTGGGCACTTCAAGGACCTTATTTCTGCTATTGGCAATTGACCTGGC 540
Db 481 TTTTCTCATGGTCTTGGGCACTTCAAGGACCTTATTTCTGCTATTGGCAATTGACCTGGC 540
QY 541 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTTA 600
Db 541 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTTA 600
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660
Db 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCGAAAGCCAGTGAAGAATGC 780
Db 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCGAAAGCCAGTGAAGAATGC 780
QY 781 ATTAGATTTAAAGTTTGTATATGGAACAACTGAAGGACTCTATTGATAGGAAAAAATAGC 840
Db 781 ATTAGATTTAAAGTTTGTATATGGAACAACTGAAGGACTCTATTGATAGGAAAAAATAGC 840
QY 841 AGTAATTGGACATCTTTTGGTGGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 841 AGTAATTGGACATCTTTTGGTGGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
QY 901 ATTGAGATGTGGTATTCCTTGGATGATGAGTGTTCACCTGGTGTGATGAAGTATATTC 960
Db 901 ATTGAGATGTGGTATTCCTTGGATGATGAGTGTTCACCTGGTGTGATGAAGTATATTC 960
QY 961 CAGAATTCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1020
Db 961 CAGAATTCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1020
QY 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080
Db 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080
QY 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140
Db 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140
QY 1141 GCTCAAAATTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1141 GCTCAAAATTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
QY 1201 ATTAGCATCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
```


Db 1201 ATTACATTCTTACAAAGCAATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260

QY 1261 GATTGAAGGAGATGATGAGAAATCTTATCCAGGGACCAACATTAACACAAACCAATCAACA 1320

Db 1261 GATTGAAGGAGATGATGAGAAATCTTATCCAGGGACCAACATTAACACAAACCAATCAACA 1320

QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361

Db 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361

RESULT 5

BD242703

LOCUS

DEFINITION

BD242703 1361 bp DNA linear PAT 17-JUL-2003

Method for purifying low-density lipoprotein-associated phospholipase A2 using immobilized metal affinity chromatography.

ACCESSION

BD242703

VERSION

BD242703.1 GI:33052473

KEYWORDS

JP 2002528084-A/1.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1361)

AUTHORS

Boyd,H. and Tew,D.G.

TITLE

Method for purifying low-density lipoprotein-associated phospholipase A2 using immobilized metal affinity chromatography

JOURNAL

Patent: JP 2002528084-A 1 03-SEP-2002;

SMITHKLINE BEECHAM PLC

COMMENT

OS Homo sapiens (human)

PN JP 2002528084-A/1

PD 03-SEP-2002

PF 27-OCT-1999 JP 2000578462

PR 28-OCT-1998 GB 9823647.4,28-OCT-1998 GB 9823648.2 PI

HELEN BOYD,DAVID GRAHAM TEW

PC C12N15/09,A61P29/00,C07K1/22,C12N5/10,C12N9/16//A61K38/46, PC C12N15/00,

PC C12N5/00,A61K37/54

CC Method for purifying low-density lipoprotein-associated CC phospholipase A2

CC using immobilized metal affinity chromatography FH Key

Location/Qualifiers

FT source 1..1361

FT /organism='Homo sapiens (human)'

Location/Qualifiers

1..1361

/organism='Homo sapiens'

/mol_type='genomic DNA'

/db_xref='taxon:9606'

FEATURES

source

Query Match 100.0%; Score 1361; DB 6; Length 1361;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATGTCATGT 60

1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATGTCATGT 60

61 GCTTTTCTGCTCGGGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

61 GCTTTTCTGCTCGGGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180

121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180

181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCGGTTGGTTGTAC 240

181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATTCGGTTGGTTGTAC 240

241 AGACTTAATGTTGATCACACTAATAAGGCACTTCTTGGCTTATATATCCATCCCA 300

Db 241 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTCTTGGCTTATATATCCATCCCA 300

QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATAATTTTGGGCTTAG 360

Db 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATAATTTTGGGCTTAG 360

QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 420

Db 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 420

QY 421 GACAACTCCTGCAAACTGGAATTCCTCTCTGAGGCTGGTGAAAAATATCCACTTTGTGT 480

Db 421 GACAACTCCTGCAAACTGGAATTCCTCTCTGAGGCTGGTGAAAAATATCCACTTTGTGT 480

QY 481 TTTTCTCATGCTTGGGCAATTCAGGACACTTTTATCTGCTATTTGGCATTTGACCTGGC 540

Db 481 TTTTCTCATGCTTGGGCAATTCAGGACACTTTTATCTGCTATTTGGCATTTGACCTGGC 540

QY 541 ATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCAACTTA 600

Db 541 ATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCAACTTA 600

QY 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660

Db 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660

QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720

Db 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720

QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780

Db 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780

QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGACTCTATTGATAGGAAAAAATAGC 840

Db 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGACTCTATTGATAGGAAAAAATAGC 840

QY 841 AGTAATTTGGACATTTCTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAG 900

Db 841 AGTAATTTGGACATTTCTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAG 900

QY 901 ATTGAGATGTTGGTATTTGCTGATGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 960

Db 901 ATTGAGATGTTGGTATTTGCTGATGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCT 960

QY 961 CAGAAATTTCTCAGCCCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTCTGCTAATAT 1020

Db 961 CAGAAATTTCTCAGCCCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTCTGCTAATAT 1020

QY 1021 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACATCAGGGG 1080

Db 1021 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACATCAGGGG 1080

QY 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140

Db 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140

QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGAGCTATTGATCTTAGCAACAAGCTTC 1200

Db 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGAGCTATTGATCTTAGCAACAAGCTTC 1200

QY 1201 ATTAGCATTTTACAAAGCAATTTAGGACTTCAATAAGATTTTGTATCAGTGGGACTGCTT 1260

Db 1201 ATTAGCATTTTACAAAGCAATTTAGGACTTCAATAAGATTTTGTATCAGTGGGACTGCTT 1260

QY 1261 GATTGAAGGAGATGATGAGAAATCTTATCCAGGACCAACATTTAAACCAACCAATCAACA 1320

Db 1261 GATTGAAGGAGATGATGAGAAATCTTATCCAGGACCAACATTTAAACCAACCAATCAACA 1320

QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361

Db 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361

```
RESULT 6
AR205614
LOCUS AR205614 1361 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 9 from patent US 6369045.
ACCESSION AR205614
VERSION AR205614.1 GI:21503242
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS Macphree,C.Houston., Tew,D.Graham. and Hickey,D.Mary.Bernadette.
TITLE Phospholipase A2 inhibitors thereof and use of same in diagnosis
JOURNAL Patent: US 6369045-A 9 09-APR-2002;
FEATURES
source Location/Qualifiers
1..1361
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 1361; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCACCCAAATGTCATGT 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 61 GCTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 TCCTGTTGCCATATGAATATCAGCATGCGTCAACAAATACAAATATCAGTGGCTGC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 121 TCCTGTTGCCATATGAATATCAGCATGCGTCAACAAATACAAATATCAGTGGCTGC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 181 TGCAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCTTATCCGTTGGTTGTAC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 241 AGACTTAATGTTTGTATCAGTCACTAATAAGGGCACTTCTTGGCTTATATATFCCATCCCA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 361 CAAATTTCTTGGAACACACTGGCTTATGGCAACATTTTGAGTTACTCTTTGGTTCAAT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 421 GACAACTCCTGCAAACTGGAATCCCTCTGAGGCTGCTGTAAGAAATATCCACTTGTGT 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 481 TTTTCTCATGCTTTGGGCACTCAGGACATTTATCTGCTATTGGCAATGACCTGGC 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 541 ATCTCATGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCACTGCAACTTA 600
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGCAAAAGA 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGCAAAAGA 720
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAAGCCAGTGAAGATGC 780
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTTATTGATAGGGAATAATAGC 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 841 AGTAATTGGACATTTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 901 ATTCAGATGTTGTTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 961 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATAT 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1021 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1081 TTCAGTCCACCAGAAATTTTCTGCTGACTTCACTTTTGCAACTGGCAAAATATTTGGACACAT 1140
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1201 ATTAGCATTTCTTACAAAGCATTTAGGACTTCTATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1261 GATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAATCAACA 1320
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 7
AX006795 1361 bp DNA linear PAT 06-SEP-2000
LOCUS AX006795
DEFINITION Sequence 9 from Patent EP0974663.
ACCESSION AX006795
VERSION AX006795.1 GI:9994827
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gloger,I.S., Hickey,D.M., Macphree,C.H., Southan,C.D.,
Lawrence,G.M., Rice,S.Q. and Tew,D.G.
TITLE Lipoprotein associated phospholipase a2, inhibitors thereof and use
of same in diagnosis and therapy
JOURNAL Patent: EP 0974663-A 9 26-JAN-2000;
SMITHKLINE BEECHAM PLC (GB)
FEATURES
source Location/Qualifiers
1..1361
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 1361; DB 6; Length 1361;
```

		Best Local Similarity 100.0%; Pred. No. 0;		Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	1	1	1	1
Db	1	1	1	1	1
QY	61	1	1	1	1
Db	61	1	1	1	1
QY	121	1	1	1	1
Db	121	1	1	1	1
QY	181	1	1	1	1
Db	181	1	1	1	1
QY	241	1	1	1	1
Db	241	1	1	1	1
QY	301	1	1	1	1
Db	301	1	1	1	1
QY	361	1	1	1	1
Db	361	1	1	1	1
QY	421	1	1	1	1
Db	421	1	1	1	1
QY	481	1	1	1	1
Db	481	1	1	1	1
QY	541	1	1	1	1
Db	541	1	1	1	1
QY	601	1	1	1	1
Db	601	1	1	1	1
QY	661	1	1	1	1
Db	661	1	1	1	1
QY	721	1	1	1	1
Db	721	1	1	1	1
QY	781	1	1	1	1
Db	781	1	1	1	1
QY	841	1	1	1	1
Db	841	1	1	1	1
QY	901	1	1	1	1
Db	901	1	1	1	1
QY	961	1	1	1	1
Db	961	1	1	1	1
QY	1021	1	1	1	1
Db	1021	1	1	1	1

Db	1021	CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAATCAGGGG	1080
QY	1081	TTGAGTCCACCAGAAATTTTGCTGACTTCACTTTTGCNACTGGCAAAATAATTGGACACAT	1140
Db	1081	TTGAGTCCACCAGAAATTTTGCTGACTTCACTTTTGCNACTGGCAAAATAATTGGACACAT	1140
QY	1141	GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTC	1200
Db	1141	GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTC	1200
QY	1201	ATTAGCATCTTACAAAAGCATTTAGGACTTTCATAAAGATTTTGTGATCAGTGGGACTGCTT	1260
Db	1201	ATTAGCATCTTACAAAAGCATTTAGGACTTTCATAAAGATTTTGTGATCAGTGGGACTGCTT	1260
QY	1261	GATTGAAGGAGATGATGAGAATCTTATTCAGGGACCAACATTAAACAACAATCAACA	1320
Db	1261	GATTGAAGGAGATGATGAGAATCTTATTCAGGGACCAACATTAAACAACAATCAACA	1320
QY	1321	CATCATGTTACAGAACTCTTCAGGAATAGAGAAATCAAAAT	1361
Db	1321	CATCATGTTACAGAACTCTTCAGGAATAGAGAAATCAAAAT	1361
RESULT 8			
AX335487			
LOCUS	AX335487	1561 bp	DNA linear PAT 09-JAN-2002
DEFINITION	Sequence 5996 from Patent WO0194629.		
ACCESSION	AX335487		
VERSION	AX335487.1	GI:18126206	
KEYWORDS	.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,		
JOURNAL	Horrigan, S., Soppet, D.R. and Weaver, Z.		
FEATURES	Cancer gene determination and therapeutic screening using signature		
source	gene sets		
	Patent: WO 0194629-A 5996 13-DEC-2001;		
	Avalon Pharmaceuticals (US)		
	Location/Qualifiers		
	1..1561		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Query Match	100.0%;	Score 1361;	DB 6; Length 1561;
Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 1361;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	1	1
Db	180	1	1
QY	61	1	1
Db	240	1	1
QY	121	1	1
Db	300	1	1
QY	181	1	1
Db	360	1	1
QY	241	1	1
Db	420	1	1
QY	301	1	1

Db 480 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTTAG 539
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 420
Db 540 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 599
QY 421 GACAACTCTGCAAACTGGAATCCCTCTGAGGCTGGTGAAATAATCCACTTTGT 480
Db 600 GACAACTCTGCAAACTGGAATCCCTCTGAGGCTGGTGAAATAATCCACTTTGT 659
QY 481 TTTTCTCATGGCTTGGGGCAATCAGGACACTTTATCTGCTATTTGGCAATGACCTGGC 540
Db 660 TTTTCTCATGGCTTGGGGCAATCAGGACACTTTATCTGCTATTTGGCAATGACCTGGC 719
QY 541 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTGCAACTTA 600
Db 720 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTGCAACTTA 779
QY 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGACAAGTCTTTGGCTCTACCTTAGAAC 660
Db 780 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGACAAGTCTTTGGCTCTACCTTAGAAC 839
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 840 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 899
QY 721 ATGTTCCCAAGCTCTCAGTCTGATCTTGTGACATGATCATGGAAGCCAGTGAAGATGC 780
Db 900 ATGTTCCCAAGCTCTCAGTCTGATCTTGTGACATGATCATGGAAGCCAGTGAAGATGC 959
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACTGGAAGCACTTATGATAGGGAAAAATAGC 840
Db 960 ATTAGATTTAAAGTTTGATATGGAACAACTGGAAGCACTTATGATAGGGAAAAATAGC 1019
QY 841 AGTAATTGGACATCTTTTGGTGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 1020 AGTAATTGGACATCTTTTGGTGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG 1079
QY 901 ATTGAGATGTGGTATGCTCCCTGGATGATGGATGTTTCCACTGGGTGATGAATATTC 960
Db 1080 ATTGAGATGTGGTATGCTCCCTGGATGATGGATGTTTCCACTGGGTGATGAATATTC 1139
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTGCTTAATAT 1020
Db 1140 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTGCTTAATAT 1199
QY 1021 CATAAAAATGAAAAATGCTACTCCTGTATGATAAGAAAGAAAGATGATTACAAATCAGGG 1080
Db 1200 CATAAAAATGAAAAATGCTACTCCTGTATGATAAGAAAGAAAGATGATTACAAATCAGGG 1259
QY 1081 TTCAGTCCACCAAGATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140
Db 1260 TTCAGTCCACCAAGATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1319
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1320 GCTCAAAATTAAGGGAGACATAGATTCAAATGAGCTATTGATCTTAGCAACAAAGCTTC 1379
QY 1201 ATTAGCATTTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTGATGAGTGGACTGCTT 1260
Db 1380 ATTAGCATTTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTGATGAGTGGACTGCTT 1439
QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGAACCAACATTAAACCAACCAATCAACA 1320
Db 1440 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGAACCAACATTAAACCAACCAATCAACA 1499
QY 1321 CATCATGTTACGAACTCTTTCAGGAATAGAGAAATACAAATT 1361
Db 1500 CATCATGTTACGAACTCTTTCAGGAATAGAGAAATACAAATT 1540

HSU24577
LOCUS Human LDL-phospholipase A2 mRNA linear PRI 24-JUL-1996
DEFINITION Human LDL-phospholipase A2 mRNA, complete cds.
ACCESSION U24577
VERSION U24577.1 GI:1314245
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1561)
AUTHORS Tew,D.G., Southan,C., Rice,S.Q., Lawrence,M.P., Li,H., Boyd,H.F.,
Moore,K., Gloger,I.S. and Macphie,C.H.
TITLE Purification, properties, sequencing, and cloning of a
lipoprotein-associated, serine-dependent phospholipase involved in
the oxidative modification of low-density lipoproteins
JOURNAL Arterioscler. Thromb. Vasc. Biol. 16 (4), 591-599 (1996)
MEDLINE 96197208
PUBMED 8624782
REFERENCE 2 (bases 1 to 1561)
AUTHORS Rice,S.Q.J.
TITLE Direct Submission
JOURNAL Submitted (10-APR-1995) Simon Q.J. Rice, SmithKline Beecham
Pharmaceuticals, New Frontiers Science Park North, Third Avenue,
Harlow, Essex CM195AW, UK
COMMENT On May 16, 1996 this sequence version replaced gi:790655.
FEATURES
source
1. .1561
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="6"
/cell_type="T cell"
/tissue_type="lymphoma"
/dev_stage="adult"
217. .1542
/function="oxidized modification of low density
lipoprotein"
/note="PAP-acetylhydrolase"
/codon_start=1
/product="LDL-phospholipase A2"
/protein_id="AAB04170.1"
/db_xref="GI:1314246"
/translation="MVPPKLVHFLCLGCLAVVYFDFWQYINPVAHMKSSAWNKIQV
LMAAASFGQTKIPRGNPGYSGCTDLMFDHTNKGTFRLRYYPQSDNDRLDTLWPNKE
YFGLSKFLGTHLWLMGNILRLFLGSMTPANWNSPLRPGKPYPLVVFVSHGLGAPRTLY
SAIGIDLASHGFIVAAVEHRDRSASATYYFKDQSAEIGDKSWLYLRTLKQEEETHIR
NEQVRQRAKESQALSILIDIDHGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSPGG
ATVIQTLSEDRFCRGIALDAWEPGLGDEVYSRIPOQLFFINSEFYQYPANIIKMKKC
YSPDKERKMITIRGSHVQNFADTFATGKIIGHMLKLKGDIDSNAAIDLNSKASLAFL
QKHLGLHKDFDQWDCLIEGDDENLIPGTNINTNQHIMLQNSSGIEKYN"
813. .828
misc_feature
/note="encodes lipase motif"
polyA_site
1561
/note="18 A nucleotides"
ORIGIN
Query Match 100.0%; Score 1361; DB 9; Length 1561;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCAAAATTCATGT 60
Db 180 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCAAAATTCATGT 239
QY 61 GCTTTTCTGCTCTGCGGCTGCCTGGCTGGTGTATCTTTTGTGCTGGCAATACATAA 120
Db 240 GCTTTTCTGCTCTGCGGCTGCCTGGCTGGTGTATCTTTTGTGCTGGCAATACATAA 299
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
Db 300 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 359

QY 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCTTATTCCGTTGGTTGTAC 240
Db 360 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCTTATTCCGTTGGTTGTAC 419
QY 241 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTATCCATCCCA 300
Db 420 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTATCCATCCCA 479
QY 301 AGATAATGATCGCCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 480 AGATAATGATCGCCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 539
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 540 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 599
QY 421 GACAACTCTGCAAACTGGAATTCCTCTCTGAGGCTGGTGAAATAATATCCACTTGTGT 480
Db 600 GACAACTCTGCAAACTGGAATTCCTCTCTGAGGCTGGTGAAATAATATCCACTTGTGT 659
QY 481 TTTTCTCATGGTCTTGGGCAATTCAGGACATTTATTTCTGCTATTTGGCAATTCGACCTGGC 540
Db 660 TTTTCTCATGGTCTTGGGCAATTCAGGACATTTATTTCTGCTATTTGGCAATTCGACCTGGC 719
QY 541 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTTA 600
Db 720 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTTA 779
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGCAAGTCTTTGGCTCTACCTTAGAAC 660
Db 780 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGCAAGTCTTTGGCTCTACCTTAGAAC 839
QY 661 CCTGAAACAAGAGGAGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 840 CCTGAAACAAGAGGAGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 899
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTCATGGAAGCCAGTGGAAGATGC 780
Db 900 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTCATGGAAGCCAGTGGAAGATGC 959
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGACTCTATTGATAGGGAAATAATAGC 840
Db 960 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGACTCTATTGATAGGGAAATAATAGC 1019
QY 841 AGTAATTGGACATTTCTTTTGGTGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 1020 AGTAATTGGACATTTCTTTTGGTGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG 1079
QY 901 ATTGAGATGTGGTATGCCCCTGGATGCATGGATGTTTCCACTGGTGATGAAGTATATTC 960
Db 1080 ATTGAGATGTGGTATGCCCCTGGATGCATGGATGTTTCCACTGGTGATGAAGTATATTC 1139
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAAATATTTCCAAATATCCTGCTAATAT 1020
Db 1140 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAAATATTTCCAAATATCCTGCTAATAT 1199
QY 1021 CATAAAATGAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db 1200 CATAAAATGAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAATCAGGGG 1259
QY 1081 TTCAGTCCACCAGAAATTTTGCTGACTTCATTTTGCAACTGGCAAAATAATTTGGACACAT 1140
Db 1260 TTCAGTCCACCAGAAATTTTGCTGACTTCATTTTGCAACTGGCAAAATAATTTGGACACAT 1319
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1320 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1379
QY 1201 ATTAGCATTTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1380 ATTAGCATTTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1439
QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTCCAGGGACCAACATTAAACAAATCAACA 1320

Db 1440 GATTGAAGGAGATGATGAGAAATCTTATTTCCAGGACCAACATTAAACCAATCAACA 1499
QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361
Db 1500 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1540
RESULT 10
CQ717247
LOCUS CQ717247 1505 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 3181 from Patent WO02068579.
ACCESSION CQ717247
VERSION CQ717247.1 GI:42278104
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 3181 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1 .1505
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 99.9%; Score 1359.4; DB 6; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTTGATGT 60
Db 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTTGATGT 184
QY 61 GCTTTTCTGCTCTGCGGCTGCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATAAA 120
Db 185 GCTTTTCTGCTCTGCGGCTGCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATAAA 244
QY 121 TCCTGTTGCCATATGAAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
Db 245 TCCTGTTGCCATATGAAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCTTATTTCCGTTGGTTGTAC 240
Db 305 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCTTATTTCCGTTGGTTGTAC 364
QY 241 AGACTTAATGTTTGATCACACTTAATAAGGGCACCTTCTTGCGTTTATATTATCCATCCCA 300
Db 365 AGACTTAATGTTTGATCACACTTAATAAGGGCACCTTCTTGCGTTTATATTATCCATCCCA 424
QY 301 AGATAATGATCGCCTTGACACCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCCTTGACACCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544
QY 421 GACAACTCTGCAAACTGGAATTTCCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT 480
Db 545 GACAACTCTGCAAACTGGAATTTCCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT 604
QY 481 TTTTCTCATGGTCTTGGGGCAATTCAGGACACTTTATTTCTGCTATTGGCATTGACCTGGC 540
Db 605 TTTTCTCATGGTCTTGGGGCAATTCAGGACACTTTATTTCTGCTATTGGCATTGACCTGGC 664

QY 541 ATCTCATGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db |||||||
QY 665 ATCTCATGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724
Db |||||||
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 660
Db |||||||
QY 725 CTATTTCAAGGACCAATCTGCTGCAGAAACAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 784
Db |||||||
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGCAAAAGA 720
Db |||||||
QY 785 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGCAAAAGA 844
Db |||||||
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
Db |||||||
QY 845 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 904
Db |||||||
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840
Db |||||||
QY 905 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 964
Db |||||||
QY 841 AGTAATTGGACATTTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db |||||||
QY 965 AGTAATTGGACATTTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
Db |||||||
QY 901 ATTAGATGTGGTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db |||||||
QY 1025 ATTAGATGTGGTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
Db |||||||
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCCTGCTAATAT 1020
Db |||||||
QY 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCCTGCTAATAT 1144
Db |||||||
QY 1021 CATAAAATGAANAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACATCAGGGG 1080
Db |||||||
QY 1145 CATAAAATGAANAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACATCAGGGG 1204
Db |||||||
QY 1081 TTCAGTCCACCAGAAATTTTGGTCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACAT 1140
Db |||||||
QY 1205 TTCAGTCCACCAGAAATTTTGGTCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACAT 1264
Db |||||||
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGAGCTATTGATCTTTAGCAACAAGCTTC 1200
Db |||||||
QY 1265 GCTCAAAATTAAGGGAGACATAGATTCAAAATGAGCTATTGATCTTTAGCAACAAGCTTC 1324
Db |||||||
QY 1201 ATTAGCATTTCTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db |||||||
QY 1325 ATTAGCATTTCTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384
Db |||||||
QY 1261 GATTGAAGGAGATGATGAGAACTTTATCCAGGGACCAACATTAACACAACCAATCAACA 1320
Db |||||||
QY 1385 GATTGAAGGAGATGATGAGAACTTTATCCAGGGACCAACATTAACACAACCAATCAACA 1444
Db |||||||
QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361
Db |||||||
QY 1445 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1485
Db |||||||

RESULT 11
HSU20157
LOCUS 1505 bp mRNA linear PRI 21-APR-1995
DEFINITION Human platelet-activating factor acetylhydrolase mRNA, complete cds.
ACCESSION U20157
VERSION U20157.1 GI:780132
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1505)
AUTHORS Tjoelker, L.W., Wilder, C., Eberhardt, C., Stafforini, D.M.,
Dietsch, G., Schimpf, B., Hooper, S., Trong, H., Cousins, L.S.,
Zimmerman, G.A., Yamada, Y., McIntyre, T.M., Prescott, S.M. and

Gray, P.W.
Anti-inflammatory properties of a platelet-activating factor
acetylhydrolase
Nature 374 (6522), 549-553 (1995)
95214779
7700381
2 (bases 1 to 1505)
Tjoelker, L.W.
Direct Submission
Submitted (20-JAN-1995) Larry W. Tjoelker, ICOS Corporation, 22021
20th Ave. S.E., Bothell, WA 98021, USA
Location/Qualifiers
1. 1505
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SAH 406-3"
/cell_type="macrophage"
/tissue_type="myeloid"
/clone_lib="in vitro differentiated macrophage cDNA
library"
162. 1487
/codon_start=1
/product="platelet-activating factor acetylhydrolase"
/protein_id="AAC50126.1"
/db_xref="GI:780133"
/translation="MVPKLVHLCGCLAVVYVFDWQYINPVAHMKSSAWNKIQV
LMAAASFQTKIPRGNGPYSGCTDLMFHTNKGTLRLYYPSQDNDRDLTLIPNKE
YFWGLSKFLGTHWLMGNILRLFLGSMTPANWNSPLRPGKYLPLVVFSLGLGAPRTLY
SAIGIDLASHGFIVAAVEHRDRSASATYFKDQSAAEIGDKSWLYLRLTKQEEETHIR
NEQVRQAKESQALSILIDIDHGKPKVKNALDKPDMQQLKSIDREKIAVIGHSFGG
ATVIQTLSEDFRCGIALDAWMPFLGDEVYSRIPOPLFFINSEYFQYPANIKMKKC
YSPDKERKMITIRGSVHONFADFTFATGKIIGHMLKLKGDIDSNVAIDLKSLAFL
QKHLGLHKDFQWDCLEGGDENLIPGTNINTNQHIMLQNSSGIEKYN"
ORIGIN

Query Match 99.9%; Score 1359.4; DB 9; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTCCCAACCAATTCATGT 60
Db |||||||
QY 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTCCCAACCAATTCATGT 184
Db |||||||
QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTTATCCTTTTGACTGGCAATACATAA 120
Db |||||||
QY 185 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTTATCCTTTTGACTGGCAATACATAA 244
Db |||||||
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAGTACTGATGGCTGC 180
Db |||||||
QY 245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAGTACTGATGGCTGC 304
Db |||||||
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCTTATTCCTGTTGGTTGTAC 240
Db |||||||
QY 305 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCTTATTCCTGTTGGTTGTAC 364
Db |||||||
QY 241 AGACTTAATGTTTGATCACAATAAAGGCACCTTCTTCGGTTTATATATCCATCCCA 300
Db |||||||
QY 365 AGACTTAATGTTTGATCACAATAAAGGCACCTTCTTCGGTTTATATATCCATCCCA 424
Db |||||||
QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db |||||||
QY 425 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484
Db |||||||
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db |||||||
QY 485 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544
Db |||||||
QY 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT 480
Db |||||||
QY 545 GACAACTCTGCAAACTGGAATTCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT 604
Db |||||||
QY 481 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATCTGCTATTGGGCATTCACCTGGC 540
Db |||||||

Db 605 TTTTCTCATGGTCTGGGGCATTCAGGACACTTTATTCTGCTATTGGCATTGACTGGC 664
Qy 541 ATCTCATGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGTCATCTGCAACTTA 600
Db 665 ATCTCATGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGTCATCTGCAACTTA 724
Qy 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAAAGTCTTGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAAAGTCTTGCTCTACCTTAGAAC 784
Qy 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGCAAAAGAGCAAAAGA 720
Db 785 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGCAAAAGAGCAAAAGA 844
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATCATGGAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATCATGGAAGCCAGTGAAGATGC 904
Qy 781 ATTAGATTAAAGTTTGATATGGAACAACCTGAAGCACTCTATTGATAGGGAAAAATAGC 840
Db 905 ATTAGATTAAAGTTTGATATGGAACAACCTGAAGCACTCTATTGATAGGGAAAAATAGC 964
Qy 841 AGTAATTGGACATTCTTTTGGTGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 965 AGTAATTGGACATTCTTTTGGTGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
Qy 901 ATTAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
Qy 961 CAGAAATTCCTCAGCCCCCTCTTTTATTATCAACTCTGAATATTTTCAATATCCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCCCTCTTTTATTATCAACTCTGAATATTTTCAATATCCTGCTAATAT 1144
Qy 1021 CATAAAAATGAAAAATGCTACTACCTGTATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db 1145 CATAAAAATGAAAAATGCTACTACCTGTATAAAGAAAGAAAGATGATTACAATCAGGGG 1204
Qy 1081 TTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140
Db 1205 TTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1264
Qy 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCACTATTGATCTTAGCAACAAAGCTTC 1200
Db 1265 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCACTATTGATCTTAGCAACAAAGCTTC 1324
Qy 1201 ATTAGCATTTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTGATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATTTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTGATCAGTGGGACTGCTT 1384
Qy 1261 GATTGAAGGAGATGATGAGAAATCTTATCCAGGGACCAACATTAAACACAACTCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAAATCTTATCCAGGGACCAACATTAAACACAACTCAACA 1444
Qy 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATPACAAAT 1361
Db 1445 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATPACAAAT 1485

RESULT 12
A81377

LOCUS A81377 1520 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 7 from Patent WO9909147.
ACCESSION A81377
VERSION A81377.1 GI:6731692
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1520)
AUTHORS Eberhardt,C.D. and Gray,P.
TITLE TRUNCATED PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE

JOURNAL Patent: WO 9909147-A 7 25-FEB-1999;
ICOS CORP (US)
FEATURES Location/Qualifiers
source 1..1520
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
CDS 162..1487
/note="unnamed protein product"
/codon_start=1
/protein_id="CAB69183.1"
/db_xref="GI:6731693"
/translation="MVPFKLHVLFCGLAVVYFDFQYINPVAHMKSSAWNKIQV
LMAAASFGQTKIPRGNGPYSGCTDLMFDTNKGTFELRYYPQDNDRDLDTLWIPNKE
YFWGLSKFLGTHWLMGNILRLFLGSMTPPANWNSPLRPEKYPPLVVFHSLGAFRTLY
SAIGIDLASHGFIVAAVEHRDRSASATYFFKDQSAAEIGDKSWLYLRLTKQEEETHIR
NEQVRQAKESQALSILIDIDHGKPVKNALDLKFDNMQDKSIDREKIAVIGHSGFG
ATVIQTLSEDOFRFCIGALDAWMFPLDEVYSRIPQLFFINSEYFOYPANIIKMKKC
YSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLAF
QKHLGLHKDFDQWDCLIEGDDENLIPGNTNNTNQHIMLQNSSGIEKYN"
ORIGIN
Query Match 99.9%; Score 1359.4; DB 6; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTCATGT 184
Qy 61 GCTTTTCTGCCTCTCGCGCTGCCTGCTGTGTTTATCTTTTGTGCTGGCAATACATAAA 120
Db 185 GCTTTTCTGCCTCTCGCGCTGCCTGCTGTGTTTATCTTTTGTGCTGGCAATACATAAA 244
Qy 121 TCCTGTTGCCCATATGAAATCATCATCAGCATGGGTCAACAACAAATACAAGTACTGATGCTGC 180
Db 245 TCCTGTTGCCCATATGAAATCATCATCAGCATGGGTCAACAACAAATACAAGTACTGATGCTGC 304
Qy 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGCCCTATTCCGTTGGTTGTAC 240
Db 305 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGCCCTATTCCGTTGGTTGTAC 364
Qy 241 AGACTTAATGTTTGATCACACTAATAAGGACCTTCTTTCGTTTATATATCCATCCCA 300
Db 365 AGACTTAATGTTTGATCACACTAATAAGGACCTTCTTTCGTTTATATATCCATCCCA 424
Qy 301 AGATAATGATCGCCTTGACACCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCCTTGACACCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 544
Qy 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT 480
Db 545 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT 604
Qy 481 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATCTGCTATTGGCATTTGACCTGGC 540
Db 605 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATCTGCTATTGGCATTTGACCTGGC 664
Qy 541 ATCTCATGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGTCATCTGCAACTTA 600
Db 665 ATCTCATGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGTCATCTGCAACTTA 724
Qy 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAAAGTCTTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAAAGTCTTTGGCTCTACCTTAGAAC 784
Qy 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGCAAAAGAGCAAAAGA 720
Db 785 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGCAAAAGAGCAAAAGA 844

REFERENCE 1 (bases 1 to 1520)
AUTHORS Cousens,L.S., Eberhardt,C.D., Gray,P., Trong,H.Le., Tjoelker,L.W.
and Wilder,C.L.
TITLE Platelet-activating factor acetylhydrolase
JOURNAL Patent: US 6146625-A 7 14-NOV-2000;
FEATURES Location/Qualifiers
source 1..1520
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 99.9%; Score 1359.4; DB 6; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAATTGCATGT 60
Db 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAATTGCATGT 184
QY 61 GCTTTTCTGCTCTGCGGCTGCGCTGGCTGTGGTTTATCCCTTTGACTGGCAATACATAAA 120
Db 185 GCTTTTCTGCTCTGCGGCTGCGCTGGCTGTGGTTTATCCCTTTGACTGGCAATACATAAA 244
QY 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180
Db 245 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTAAATFCCCGGGGAAATGGGCTTATTCGGTTGTTGTAC 240
Db 305 TGCAAGCTTTGGCCAAACTAAATFCCCGGGGAAATGGGCTTATTCGGTTGTTGTAC 364
QY 241 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTTATCCATCCCA 300
Db 365 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTTATCCATCCCA 424
QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAAAATAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAAAATAAGAAATATTTTGGGGTCTTAG 484
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544
QY 421 GACAACTCCTGCAAACTGGAATTCCTCCTCTGAGGCTGGTGAAATAATCCACTTGTGT 480
Db 545 GACAACTCCTGCAAACTGGAATTCCTCCTCTGAGGCTGGTGAAATAATCCACTTGTGT 604
QY 481 TTTTCTCATGGTCTTGGGGCAATTCAGGACACTTTTATTTCTGCTATTGGCACTGGC 540
Db 605 TTTTCTCATGGTCTTGGGGCAATTCAGGACACTTTTATTTCTGCTATTGGCACTGGC 664
QY 541 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db 665 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 784
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAAGA 720
Db 785 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAAGA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTGATCATGGAAGCCAGTGAAGAATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTGATCATGGAAGCCAGTGAAGAATGC 904
QY 781 ATTAGATTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGGAAAAAATAGC 840
Db 905 ATTAGATTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGGAAAAAATAGC 964
QY 841 AGTAATTGGACATTCTTTGGTGGAGCAACGGTTTATTCAGACTCTTAGTGAAGTCAGAG 900

Db 965 AGTAATTGGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
QY 901 ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAAATATTTCCAATATCCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAAATATTTCCAATATCCTGCTAATAT 1144
QY 1021 CATAAAAATGAAAAATGCTACTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db 1145 CATAAAAATGAAAAATGCTACTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGG 1204
QY 1081 TTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACAT 1140
Db 1205 TTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACAT 1264
QY 1141 GCTCAAAATTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACCAAAGCTTC 1200
Db 1265 GCTCAAAATTAAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTAGCAACCAAAGCTTC 1324
QY 1201 ATTAGCATTTCTTACAAAAGCATTTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATTTCTTACAAAAGCATTTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGAACTCTTATTCCAGGGACCAACATTAAACACAAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAACTCTTATTCCAGGGACCAACATTAAACACAAACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1485

Search completed: March 15, 2005, 20:51:06
Job time : 6507.04 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:16 ; Search time 881.202 Seconds
(without alignments)
9142.928 Million cell updates/sec

Title: US-09-922-067f-9
Perfect score: 1361
Sequence: 1 tgagagactaagctgaact.....aggaatagagaatacaatt 1361

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues 8780412
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1361	100.0	1361	2	AAQ81780
2	1361	100.0	1361	3	AAA52357
3	1361	100.0	1561	6	ABL67659 Oesophagu
4	1359.4	99.9	1505	6	ABK92177 Prostate
5	1359.4	99.9	1505	11	ADP64943 Human pho
6	1359.4	99.9	1505	11	ADP65357
7	1359.4	99.9	1505	12	ADH43822 Human pla
8	1359.4	99.9	1505	12	ADJ74586
9	1359.4	99.9	1505	12	ADP12846 Reference
10	1359.4	99.9	1505	13	ADR25259 Breast ca
11	1359.4	99.9	1505	13	ADR14276 Human NF-
12	1359.4	99.9	1505	13	ADP54610 Human PRO
13	1359.4	99.9	1505	13	ADP23966 PRO polyp
14	1359.4	99.9	1520	2	AAQ87947
15	1359.4	99.9	1520	2	AAT80564 Human pla
16	1359.4	99.9	1520	2	AAT87048 Human pla
17	1359.4	99.9	1520	2	AAT96127 Human pla
18	1359.4	99.9	1520	2	AAx08463
19	1359.4	99.9	1520	2	AAV08534 Human PAF
20	1359.4	99.9	1520	3	AAA10861

21	1359.4	99.9	1520	3	AAZ24240	Human PAF
22	1359.4	99.9	1520	3	AAA59579	CDNA enco
23	1359.4	99.9	1520	4	AA04143	Human pla
24	1359.4	99.9	1520	4	AAC89057	Platelet-
25	1359.4	99.9	1520	5	AA24719	Human pla
26	1359.4	99.9	1520	9	ADA19490	Human pla
27	1357.4	99.7	1520	2	AAT63701	CDNA enco
28	1323	97.2	1323	6	AA36733	Human lip
29	1247.8	91.7	1320	4	AA04169	Mouse-Hum
30	1199.4	88.1	1203	10	ADG73659	Human PAF
31	1198.4	88.1	1563	10	ADG73667	Human hCB
32	1198.4	88.1	1917	10	ADG73669	Human GCB
33	1198.4	88.1	1929	10	ADG73671	Human aCB
34	1172.6	86.2	1320	4	AA04168	Mouse-Hum
35	1162.4	85.4	1335	2	AAT87072	Human pla
36	1162.4	85.4	1335	3	AAA10885	Synthetic
37	1162.4	85.4	1335	3	AAZ24261	Human PAF
38	1162.4	85.4	1335	4	AA04165	Human pla
39	1162.4	85.4	1335	4	AAC89078	Platelet-
40	1162.4	85.4	1335	5	AA24740	Human pla
41	1151.4	84.6	1336	9	ADA19513	CDNA rela
42	1049.6	77.1	1528	9	ADA19506	Cow plasm
43	1049.6	77.1	1533	2	AAT87066	Bovine pl
44	1049.6	77.1	1533	2	AAx08478	Bovine pl
45	1049.6	77.1	1533	2	AAV08552	Bovine PA

ALIGNMENTS

RESULT 1
AAQ81780
ID AAQ81780 standard; cDNA; 1361 BP.

XX AAQ81780;

DT 25-MAR-2003 (revised)

DT 18-AUG-1995 (first entry)

XX Human T-cell lymphoma lipoprotein-associated phospholipase-A2.

XX T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2; enzyme;
KW atherosclerosis; diagnosis; therapy; antiarteriosclerotic; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 38..1357
FT /*tag= a

XX WO9500649-A1.

XX 05-JAN-1995.

XX 24-JUN-1994; 94WO-GB001374.

XX 25-JUN-1993; 93GB-00013144.

XX 11-JAN-1994; 94GB-00000413.

(SMIK) SMITHKLINE BEECHAM PLC.

XX Macphee CH, Tew DG, Southan CD, Hickey DMB, Gloger IS;
PI Lawrence GMP, Rice SQJ;

XX WPI; 1995-052086/07.

XX P-PSDB; AAR64928.

XX Purified lipoprotein associated phospholipase A2 - used to develop prods.
PT for diagnosis and therapy, partic. inhibitors for treatment of
PT atherosclerosis.

XX Claim 8; Page 19; 29pp; English.

Db 1020 AGTAATTGGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 1079
Qy 901 ATTCAGATGTGGTATTGCCCTGGATGATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1080 ATTCAGATGTGGTATTGCCCTGGATGATGGATGTTTCCACTGGGTGATGAAGTATATTC 1139
Qy 961 CAGAATTCCTCAGCCCCCTCTTTTATCAACTCTGAAATATTTCCAATATCTCTGTAATAT 1020
Db 1140 CAGAATTCCTCAGCCCCCTCTTTTATCAACTCTGAAATATTTCCAATATCTCTGTAATAT 1199
Qy 1021 CATAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGG 1080
Db 1200 CATAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGG 1259
Qy 1081 TTCAGTCCACAGAAATTTTGTGACTTCACTTTTGCACTGGCAAAATAAATTTGGACACAT 1140
Db 1260 TTCAGTCCACAGAAATTTTGTGACTTCACTTTTGCACTGGCAAAATAAATTTGGACACAT 1319
Qy 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1320 GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1379
Qy 1201 ATTAGCAATCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1380 ATTAGCAATCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1439
Qy 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGACCAACATTAACACAAACCAATCAACA 1320
Db 1440 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGACCAACATTAACACAAACCAATCAACA 1499
Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1500 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1540

RESULT 4
ABK92177
ID ABK92177 standard; DNA; 1505 BP.
XX AC ABK92177;
XX AC
XX 15-AUG-2002 (first entry)
XX Prostate cancer-associated DNA sequence #63.
DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
XX gene therapy; gene; ds.
KW Mammalia.
XX
XX WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
PI
XX WPI; 2002-471335/50.
DR P-PSDB; ABG61862.

XX Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX Claim 22; Page 347; 436pp; English.
PS
XX The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;
Query Match 99.9%; Score 1359.4; DB 6; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 184
Qy 61 GCTTTTCTGCCTCTCGGCTGCCTGGCTGCTGCTTTATCCTTTTGACTGGCAATACATAA 120
Db 185 GCTTTTCTGCCTCTCGGCTGCCTGGCTGCTGCTTTATCCTTTTGACTGGCAATACATAA 244
Qy 121 TCCTGTGCCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGC 180
Db 245 TCCTGTGCCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGC 304
Qy 181 TGCAAGCTTTGGCCAACTAAATCCCGCGGGAAATGGGCCCTTATTCGTTGGTTGTAC 240
Db 305 TGCAAGCTTTGGCCAACTAAATCCCGCGGGAAATGGGCCCTTATTCGTTGGTTGTAC 364
Qy 241 AGACTTAATGTTTGATCACACTAATAAGGCACCTTCTTGCGTTTATATATCCATCCCA 300
Db 365 AGACTTAATGTTTGATCACACTAATAAGGCACCTTCTTGCGTTTATATATCCATCCCA 424
Qy 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484
Qy 361 CAAATTTCTTGGAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544
Qy 421 GACAACTCTGCAAACTGGAATCCCTCTGAGGCCCTGGTGAATAATATCCACTTGTGT 480
Db 545 GACAACTCTGCAAACTGGAATCCCTCTGAGGCCCTGGTGAATAATATCCACTTGTGT 604
Qy 481 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTTATCTGCTATTGGCAATGACCTGGC 540
Db 605 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTTATCTGCTATTGGCAATGACCTGGC 664
Qy 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCTGCAACTTA 600
Db 665 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCTGCAACTTA 724
Qy 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAACTCTTGCTCTACCTTAGAAC 660

Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAAAGTCTTGGCTCTACCTTAGAAC 784
Qy 661 CCTGAAACAAGAGGAGGACACATATACGAAATAGCAGGTACGGCAAGAGCAAAAGA 720
Db 785 CCTGAAACAAGAGGAGGACACATATACGAAATAGCAGGTACGGCAAGAGCAAAAGA 844
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTTGACATTTGATCATGGAAGCCAGTGAAGATGC 904
Qy 781 ATTAGATTAAAGTTTGATATGGAACAACACTGAAGGACTCTATTGATAGGAAAAATAGC 840
Db 905 ATTAGATTAAAGTTTGATATGGAACAACACTGAAGGACTCTATTGATAGGAAAAATAGC 964
Qy 841 AGTAATTGGACATTTCTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 900
Db 965 AGTAATTGGACATTTCTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 1024
Qy 901 ATTCAGATGTGTTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTGTTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
Qy 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCCTGCTAATAT 1144
Qy 1021 CATAAATGAAAAATGCTACTCCTCATATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db 1145 CATAAATGAAAAATGCTACTCCTCATATAAAGAAAGAAAGATGATTACAATCAGGGG 1204
Qy 1081 TTCAGTCCACCAGAAATTTTGCTGACTTCACCTTTTGCACTGGCAAAATAATTGGACACAT 1140
Db 1205 TTCAGTCCACCAGAAATTTTGCTGACTTCACCTTTTGCACTGGCAAAATAATTGGACACAT 1264
Qy 1141 GCTCAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAAGCTTC 1200
Db 1265 GCTCAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAAGCTTC 1324
Qy 1201 ATTAGCATTTTACAAAGCATTTTAGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATTTTACAAAGCATTTTAGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384
Qy 1261 GATTGAAGGAGATGATGAGAAATCTTTATCCAGGGACCAACATTAAACAAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAAATCTTTATCCAGGGACCAACATTAAACAAACCAATCAACA 1444
Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 5

ADP64943

ID ADP64943 standard; DNA; 1505 BP.

XX AC ADP64943;

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 12-AUG-2004 (first entry)

XX 31-OCT-2002; 2002WO-US035433.
PF 31-OCT-2001; 2001US-0336220P.
PR (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX Hirsch R, Thorton SL;
XX WPI; 2003-712740/67.
DR GENBANK; NM_005084.
XX Diagnosing and analyzing autoimmune disease using gene expression
PT profiles and microarray technology, useful for diagnosing and treating
PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT gout.
XX Disclosure; Page; 56pp; English.
PS The invention relates to a novel method for diagnosing and analysing
XX autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This polynucleotide
CC represents a DNA sequence relating to the genes used in the analysis and
CC treatment of autoimmune diseases or arthritides. Note: This sequence is
CC not shown in the specification. It has been supplied in an electronic
CC format from WIPO.
XX
SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.9%; Score 1359.4; DB 11; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCCAAATGTCATGT 60
Db 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCCAAATGTCATGT 184
Qy 61 GCTTTTCTGCTCTGCGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 185 GCTTTTCTGCTCTGCGGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
Qy 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAGTACTGATGGCTGC 180
Db 245 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAGTACTGATGGCTGC 304
Qy 181 TGCAAGCTTTGGCCCAACCTAAATCCCGGGGAAATGGGCTTATCCGTTGGTTGTAC 240
Db 305 TGCAAGCTTTGGCCCAACCTAAATCCCGGGGAAATGGGCTTATCCGTTGGTTGTAC 364
Qy 241 AGACTTAATGTTTGTATCACAATAAAGGACCTTCTTGGCTTTATATATATATATATATATAT 300
Db 365 AGACTTAATGTTTGTATCACAATAAAGGACCTTCTTGGCTTTATATATATATATATATATAT 424
Qy 301 AGATAATGATCGCCTTGACACCCCTTTGGATGCCAAATAAAGAAATATTTTGGGGTCTTAG 360

Db	425	AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG	484
QY	361	CAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGTTACTCTTTGGTTCAAT	420
Db	485	CAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGTTACTCTTTGGTTCAAT	544
QY	421	GACAACTCCTGCAAACTGGAATTCCTCTCTGAGGCTGGTGAAATAATATCCACTTGTGT	480
Db	545	GACAACTCCTGCAAACTGGAATTCCTCTCTGAGGCTGGTGAAATAATATCCACTTGTGT	604
QY	481	TTTTTCTCATGGTCTTGGGCAATTCAGGACACTTTATTTCTGCTATTGGCAATTCACCTGGC	540
Db	605	TTTTTCTCATGGTCTTGGGCAATTCAGGACACTTTATTTCTGCTATTGGCAATTCACCTGGC	664
QY	541	ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTGCAACTTA	600
Db	665	ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTGCAACTTA	724
QY	601	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC	660
Db	725	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC	784
QY	661	CCTGAAACAAGAGGAGGAGACACATATACGAAATGACAGGTACGGCAAGAGCAAAAGA	720
Db	785	CCTGAAACAAGAGGAGGAGACACATATACGAAATGACAGGTACGGCAAGAGCAAAAGA	844
QY	721	ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAAGCCAGTGAAGATGC	780
Db	845	ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAAGCCAGTGAAGATGC	904
QY	781	ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAAAAATAGC	840
Db	905	ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAAAAATAGC	964
QY	841	AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG	900
Db	965	AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG	1024
QY	901	ATTCAGATGTGGTATTGCCCTGGATGGATGGATGTTTCCACTGGGTGATGAAGTATATTC	960
Db	1025	ATTCAGATGTGGTATTGCCCTGGATGGATGGATGTTTCCACTGGGTGATGAAGTATATTC	1084
QY	961	CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT	1020
Db	1085	CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT	1144
QY	1021	CATAAAATGAAAAATGTACTACCTGTATAAGAAAGAAAGATGATTACAATCAGGGG	1080
Db	1145	CATAAAATGAAAAATGTACTACCTGTATAAGAAAGAAAGATGATTACAATCAGGGG	1204
QY	1081	TTCAAGTCCACCAGAAATTTTGTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACAT	1140
Db	1205	TTCAAGTCCACCAGAAATTTTGTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACAT	1264
QY	1141	GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTC	1200
Db	1265	GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTC	1324
QY	1201	ATTAGCATTTCTACAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT	1260
Db	1325	ATTAGCATTTCTACAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT	1384
QY	1261	GATTGAAGGAGATGATGAGAAATCTTATTCAGGGACCAACATTAAACAACCAATCAACA	1320
Db	1385	GATTGAAGGAGATGATGAGAAATCTTATTCAGGGACCAACATTAAACAACCAATCAACA	1444
QY	1321	CATCATGTTACAGAACTCTTTCAGGAATPAGAGAAATACAATT	1361
Db	1445	CATCATGTTACAGAACTCTTTCAGGAATPAGAGAAATACAATT	1485

ADP65357	
ID	ADP65357 standard; DNA; 1505 BP.
XX	
AC	ADP65357;
XX	
DT	12-AUG-2004 (first entry)
XX	
DE	Human platelet-activating factor acetylhydrolase mRNA, complete DNA.
XX	
KW	autoimmune disease; arthritis; gene expression analysis;
KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW	antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
KW	immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW	immune; ds; human.
XX	
OS	Homo sapiens.
XX	
PN	WO2003072827-A1.
XX	
PD	04-SEP-2003.
XX	
PF	31-OCT-2002; 2002WO-US035433.
XX	
PR	31-OCT-2001; 2001US-0336220P.
XX	
PA	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX	
PI	Hirsch R, Thorton SL;
XX	
DR	WPI; 2003-712740/67.
DR	GENBANK; U20157.
XX	
PT	Diagnosing and analyzing autoimmune disease using gene expression
PT	profiles and microarray technology, useful for diagnosing and treating
PT	rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
PT	gout.
XX	
PS	Disclosure; Page; 56pp; English.
XX	
CC	The invention relates to a novel method for diagnosing and analysing
CC	autoimmune disease or arthritides. The method comprises obtaining a
CC	patient sample containing mRNA, analysing gene expression using the mRNA
CC	that results in a gene expression signature of the mRNA, and using that
CC	gene expression signature to diagnose or analyse the autoimmune disease
CC	or arthritides in the patient, where gene expression of at least 60% of
CC	the genes correlates with that of the gene signature. The invention
CC	further comprises: a treatment of rheumatoid arthritis; identification of
CC	genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC	other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC	array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC	analyses of autoimmune disease or rheumatoid arthritis; screening the
CC	efficacy of a candidate drug in vitro for the treatment of collagen-
CC	induced arthritis; and reducing the symptoms associated with collagen-
CC	induced arthritis. The compositions of the invention have the following
CC	activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC	antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC	methods and compositions of the present invention are useful for
CC	diagnosing and treating autoimmune disease or arthritides, such as
CC	rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC	fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC	immune disease caused by an infectious agent. This polynucleotide
CC	represents a DNA sequence relating to the genes used in the analysis and
CC	treatment of autoimmune diseases or arthritides. Note: This sequence is
CC	not shown in the specification. It has been supplied in an electronic
CC	format from WIPO.
XX	
SQ	Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match	99.9%;	Score 1359.4;	DB 11;	Length 1505;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1360;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			

CC myocardial infarction, which is applicable in providing supplementary
CC information for appropriate treatment and also in the study of onset
CC mechanism. The present sequence represents a human nucleotide sequence
CC which is given in the exemplification of the present invention.
XX
SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.9%; Score 1359.4; DB 12; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCCAAAATTGTCATGT 60
Db |||||
125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCCAAAATTGTCATGT 184

QY 61 GCTTTTCTGCTCTGCGGCTGCCCTGGCTGTGTTTATCCTTTTGACTGGCAATACATAAAA 120
Db |||||
185 GCTTTTCTGCTCTGCGGCTGCCCTGGCTGTGTTTATCCTTTTGACTGGCAATACATAAAA 244

QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAACTGATGGCTGC 180
Db |||||
245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAACTGATGGCTGC 304

QY 181 TGCAAGCTTTGGCCAACTAAATCCCGCGGGAATGGGCCCTTATTCCTGTTGGTTGTAC 240
Db |||||
305 TGCAAGCTTTGGCCAACTAAATCCCGCGGGAATGGGCCCTTATTCCTGTTGGTTGTAC 364

QY 241 AGACTTAATGTTTGATCACACTAATAAGGCACCTTCTTTCGTTTATATTCATCCCA 300
Db |||||
365 AGACTTAATGTTTGATCACACTAATAAGGCACCTTCTTTCGTTTATATTCATCCCA 424

QY 301 AGATAATGATCGCCCTTGACACCCCTTGATCCCAATAAAGAAATATTTGGGCTCTAG 360
Db |||||
425 AGATAATGATCGCCCTTGACACCCCTTGATCCCAATAAAGAAATATTTGGGCTCTAG 484

QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db |||||
485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544

QY 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAAATAATCCACTTGTGT 480
Db |||||
545 GACAACTCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAAATAATCCACTTGTGT 604

QY 481 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATCTGCTATTGGCATTGACCTGGC 540
Db |||||
605 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATCTGCTATTGGCATTGACCTGGC 664

QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db |||||
665 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724

QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGCAAGTCTTGGCTCTACCTTAGAAC 660
Db |||||
725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGCAAGTCTTGGCTCTACCTTAGAAC 784

QY 661 CCTGAAACAAGAGGAGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db |||||
785 CCTGAAACAAGAGGAGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 844

QY 721 ATGTTCCCAAGCTCTCAGTCTGATCTTGACATTTGACATGATGAAAGCCAGTGAAGATGC 780
Db |||||
845 ATGTTCCCAAGCTCTCAGTCTGATCTTGACATTTGACATGATGAAAGCCAGTGAAGATGC 904

QY 781 ATTAGATTAAAGTTTGATATGAACTGAAGGACTCTATTGATAGGGGAAAAATAGC 840
Db |||||
905 ATTAGATTAAAGTTTGATATGAACTGAAGGACTCTATTGATAGGGGAAAAATAGC 964

QY 841 AGTAATTGGACATTTCTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG 900
Db |||||
965 AGTAATTGGACATTTCTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG 1024

QY 901 ATTCAGATGTGGTATTCCTGATGATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db |||||

Db 1025 ATTCAGATGTGGTATTGCCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCATATATCCTGCTATAT 1020
Db |||||
1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCATATATCCTGCTATAT 1144

QY 1021 CATAAAAATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db |||||
1145 CATAAAAATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1204

QY 1081 TTTAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACAT 1140
Db |||||
1205 TTTAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACAT 1264

QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db |||||
1265 GCTCAAAATTAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTAGCAACAAAGCTTC 1324

QY 1201 ATTAGCATTTTACAAAAGCATTTTAGGACTTTCATAAAGATTTTATGATCAGTGGACTGCTT 1260
Db |||||
1325 ATTAGCATTTTACAAAAGCATTTTAGGACTTTCATAAAGATTTTATGATCAGTGGACTGCTT 1384

QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACACAACCAATCAACA 1320
Db |||||
1385 GATTGAAGGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACACAACCAATCAACA 1444

QY 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361
Db |||||
1445 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1485

RESULT 8

ADJ74586

ID ADJ74586 standard; mRNA; 1505 BP.

XX AC ADJ74586;

XX DT 06-MAY-2004 (first entry)

XX DE Human platelet-activating factor acetylhydrolase mRNA SEQ ID NO:10.

XX KW ds; gene; human; platelet-activating factor acetylhydrolase; restenosis;

XX KW coronary angioplasty; balloon coronary angioplasty;

XX OS Homo sapiens.

XX PN WO2004015104-A1.

XX PD 19-FEB-2004.

XX PF 20-MAR-2003; 2003WO-JP003478.

XX PR 09-AUG-2002; 2002JP-00233041.

XX PA (NAGO-) NAGOYA IND SCI RES INST.

XX PA (GIFU-) GIFU INT INST BIOTECHNOLOGY.

XX PI Yamada Y, Yokota M;

XX DR WPI; 2004-180672/17.

XX PT Analysis of specific gene polymorphisms in clinical nucleic acid sample

XX PT for prediction of risk of restenosis after balloon or stent coronary

XX PT angioplasty.

XX PS Disclosure; SEQ ID NO 10; 164pp; Japanese.

XX CC The invention relates to a novel method for predicting the risk of

XX CC restenosis after coronary angioplasty comprising analysing specific gene

XX CC polymorphisms in a clinical nucleic acid sample. The method is useful for

XX CC the diagnosis of the genetic risk of restenosis following balloon or

XX CC stent coronary angioplasty. The method has high accuracy and high

CC estimation ratio. The present sequence is used in the exemplification of
CC the invention.
XX
SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.9%; Score 1359.4; DB 12; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 184

QY 61 GCTTTTCTGCTCTGCGGCTGCCCTGGCTGTGTTTATCCTTTTGACTGGCAATACATAAA 120
Db 185 GCTTTTCTGCTCTGCGGCTGCCCTGGCTGTGTTTATCCTTTTGACTGGCAATACATAAA 244

QY 121 TCCTGTGCCCCATATGAAATCATCAGCATGGGTCAACAAATACAACTACTGATGGCTGC 180
Db 245 TCCTGTGCCCCATATGAAATCATCAGCATGGGTCAACAAATACAACTACTGATGGCTGC 304

QY 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAATGGGCCTTATTCGGTTGGTTGTAC 240
Db 305 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAATGGGCCTTATTCGGTTGGTTGTAC 364

QY 241 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTATCCATCCCA 300
Db 365 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTATCCATCCCA 424

QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484

QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 544

QY 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCTGGTGAAATAATATCCACTTGTGT 480
Db 545 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCTGGTGAAATAATATCCACTTGTGT 604

QY 481 TTTTCTCATGCTCTTGGGGCATTCAGGACACTTTATCTGCTATTTGGCATTGACTGGC 540
Db 605 TTTTCTCATGCTCTTGGGGCATTCAGGACACTTTATCTGCTATTTGGCATTGACTGGC 664

QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db 665 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724

QY 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGACAAGTCTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGACAAGTCTTGGCTCTACCTTAGAAC 784

QY 661 CCTGAAACAAGAGGAGAGACACATATACGAAATGAGCAGGTACGGCAAAAGAGCAAAAGA 720
Db 785 CCTGAAACAAGAGGAGAGACACATATACGAAATGAGCAGGTACGGCAAAAGAGCAAAAGA 844

QY 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATCATGGAAAGCAGTGAAGAAATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATCATGGAAAGCAGTGAAGAAATGC 904

QY 781 ATTAGATTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGGAAATAATAGC 840
Db 905 ATTAGATTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGGAAATAATAGC 964

QY 841 AGTAATTGGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 900
Db 965 AGTAATTGGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 1024

QY 901 ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084

QY 961 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1144

QY 1021 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAAGAGATGATTACAATCAGGGG 1080
Db 1145 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAAGAGATGATTACAATCAGGGG 1204

QY 1081 TTCAGTCCACCAGAAATTTTGTGCTGACTTCACCTTTTGCAACTGGCAAAATATTTGGACACAT 1140
Db 1205 TTCAGTCCACCAGAAATTTTGTGCTGACTTCACCTTTTGCAACTGGCAAAATATTTGGACACAT 1264

QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGACGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1265 GCTCAAAATTAAGGGAGACATAGATTCAAATGACGCTATTGATCTTAGCAACAAAGCTTC 1324

QY 1201 ATTAGCATTTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATTTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384

QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGACCAACATTAACACAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAAATCTTATTCAGGACCAACATTAACACAACCAATCAACA 1444

QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 9
ADP12846
ID ADP12846 standard; DNA; 1505 BP.
XX
AC ADP12846;
XX
DT 12-AUG-2004 (first entry)
XX
DE Reference mRNA sequence #60.
XX
transplant rejection; immune system; rheumatoid arthritis; lupus;
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
XX
Homo sapiens.
XX
WO2004042346-A2.
XX
PD 21-MAY-2004.
XX
PF 24-APR-2003; 2003WO-US012946.
XX
PR 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
(EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
XX
WPI; 2004-400724/37.
XX
Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
Claim 65; SEQ ID NO 2855; 1762pp; English.
PS
XX
The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection.

CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX
SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.9%; Score 1359.4; DB 13; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCAAAATTCATGT 60
Db |||||
125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCACCAAAATTCATGT 184
QY 61 GCTTTTCGCTCTGCGGCTGCCTGGCTGTGTTTATCCTTTTGACTGGCAATACATAAA 120
Db |||||
185 GCTTTTCGCTCTGCGGCTGCCTGGCTGTGTTTATCCTTTTGACTGGCAATACATAAA 244
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAGTACTGATGGCTGC 180
Db |||||
245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAGTACTGATGGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCCCTTATTCGGTTGGTTGAC 240
Db |||||
305 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCCCTTATTCGGTTGGTTGAC 364
QY 241 AGACTTAATGTTTGATCACACTAATAAGGCGCACCTTCTTGCCTTTATATTATCCATCCA 300
Db |||||
365 AGACTTAATGTTTGATCACACTAATAAGGCGCACCTTCTTGCCTTTATATTATCCATCCA 424
QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTAG 360
Db |||||
425 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTAG 484
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTTGGTTCAAT 420
Db |||||
485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTTGGTTCAAT 544
QY 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGCTGAGAAATATCCACTTGTGT 480
Db |||||
545 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGCTGAGAAATATCCACTTGTGT 604
QY 481 TTTTCTCATGCTCTTGGGCACTTCAGGACACTTTTATCTGCTATTGGCATTGACCTGGC 540
Db |||||
605 TTTTCTCATGCTCTTGGGCACTTCAGGACACTTTTATCTGCTATTGGCATTGACCTGGC 664
QY 541 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db |||||
665 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660
Db |||||
725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 784
QY 661 CCTGAACAAGAGGAGGAGACACATATACGAAATGACAGGTACGGCAAGAGGCAAGA 720
Db |||||
785 CCTGAACAAGAGGAGGAGACACATATACGAAATGACAGGTACGGCAAGAGGCAAGA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATCGAAAGCCAGTGAAGATGC 780
Db |||||
845 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATCGAAAGCCAGTGAAGATGC 904
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGAAAAATAGC 840
Db |||||
905 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGAAAAATAGC 964
QY 841 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTTATTCAGACTCTTAGTGAAGATCAGAG 900
Db |||||
965 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTTATTCAGACTCTTAGTGAAGATCAGAG 1024

QY 901 ATTACAGATGTGGTATTGCCCTGGATGTCATGGATGTTCCACTGGGTGATGAAGTATATTC 960
Db |||||
1025 ATTACAGATGTGGTATTGCCCTGGATGTCATGGATGTTCCACTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCATATCTCTGCTAATAT 1020
Db |||||
1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCATATCTCTGCTAATAT 1144
QY 1021 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db |||||
1145 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1204
QY 1081 TTCACTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCACACTGGCAAAATAATTGGACACAT 1140
Db |||||
1205 TTCACTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCACACTGGCAAAATAATTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGAGACATAGATTCAAATGCACTATTGATCTTAGCAACAAAGCTTC 1200
Db |||||
1265 GCTCAAAATTAAGGAGACATAGATTCAAATGCACTATTGATCTTAGCAACAAAGCTTC 1324
QY 1201 ATTACATTTCTTCAAAAAGCATTTAGGACTTCTATAAGATTTTGTAGTGGGACTGCTT 1260
Db |||||
1325 ATTACATTTCTTCAAAAAGCATTTAGGACTTCTATAAGATTTTGTAGTGGGACTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGAATCTTATTCAGGACCAACATTAAACAACCAATCAACA 1320
Db |||||
1385 GATTGAAGGAGATGATGAGAATCTTATTCAGGACCAACATTAAACAACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db |||||
1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 11

ADR14276

ID ADR14276 standard; DNA; 1505 BP.

XX ADR14276;

XX ADR14276;

DT 21-OCT-2004 (first entry)

XX Human NF-kappaB pathway-associated gene SeqID277.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
KW immunosuppressive; vulnary; gene therapy; immune disorder;
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
KW viral replication; host cell survival; evasion of immune response;
KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
KW autoimmune disorder; hyper immune activity;
KW aberrant acute phase response; hypercongenital condition; birth defect;
KW necrotic lesion; wound; organ transplant rejection;
KW aberrant signal transduction; proliferating disorder; cancer;
KW HIV propagation; gene; ds; human.

OS Homo sapiens.

XX WO2004065577-A2.

PN 05-AUG-2004.

XX 13-JAN-2004; 2004WO-US0000798.

XX 14-JAN-2003; 2003US-0440068P.

XX 12-MAY-2003; 2003US-0469757P.

XX

PR

XX

DT 18-NOV-2004 (first entry)
XX Human PRO cDNA sequence SEQ ID NO:586.
XX human; PRO; immune related disease; inflammatory immune response;
KW immune response stimulation; antiallergic; antianaemic; antiarthritic;
KW antiasthmatic; antidiabetic; antiinflammatory; antipsoriatic;
KW antirheumatic; antithyroid; CNS; dermatological; gastrointestinal;
KW haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular;
KW nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic;
KW virucide; gene therapy; gene; ss.
XX Homo sapiens.
XX WO2004039956-A2.
PN 28-OCT-2003; 2003WO-US034381.
XX 13-MAY-2004.
PD 29-OCT-2002; 2002US-0422472P.
XX (GETH) GENENTECH INC.
XX Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
PI Wood WI, Wu TD;
PI WPI; 2004-376182/35.
DR P-PSDB; ADP54611.
DR
XX New PRO polynucleotides and polypeptides, useful in diagnosing
PT and treating an immune related disease, e.g. systemic lupus
PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
PT stimulating an immune response.
XX Claim 2; SEQ ID NO 586; 3009pp; English.
XX The present invention describes an isolated PRO nucleic acid (I). Also
CC described: (1) a vector comprising (1); (2) a host cell comprising the
CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
CC antibody which specifically binds to a polypeptide of (4); (7) a
CC composition of matter comprising a polypeptide of (4), an agonist or
CC antagonist of the polypeptide or an antibody that binds to the
CC polypeptide in combination with a carrier; (8) an article of manufacture
CC comprising a container, a label on the container and a composition of
CC matter of (7); (9) a method of treating an immune related disease in a
CC mammal; (10) a method for determining the presence of a PRO polypeptide
CC in a sample suspected of having the polypeptide; (11) a method of
CC diagnosing an immune related disease or an inflammatory immune response
CC in mammal; (12) a method of identifying a compound that inhibits or
CC mimics the activity of or expression of a gene encoding a PRO polypeptide
CC ; and (13) a method of stimulating the immune response in a mammal. The
CC PRO sequences have antiallergic, antianaemic, antiarthritic,
CC antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic,
CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
CC virucide activities, and can be used in gene therapy. The nucleic acid
CC (I) and the encoded polypeptides, compositions, kits and methods are
CC useful in diagnosing and treating an immune related disease and in
CC stimulating an immune response. The present sequence represents a human
CC PRO nucleotide sequence from the present invention.
XX Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;
SQ
Query Match 99.9%; Score 1359.4; DB 13; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAACTGCTCAGCTCCCAAGATGGTGCCACCAAAATTCATGT 60
|||||

Db 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCAAAATTCATGT 184
QY 61 GCTTTTCTGCTGCGGCTGCTGGCTGTGTTTATCTCTTTGACTGGCAATACATAAA 120
|||
Db 185 GCTTTTCTGCTGCGGCTGCTGGCTGTGTTTATCTCTTTGACTGGCAATACATAAA 244
|||
QY 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAACTACTGATGCTGC 180
|||
Db 245 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAACTACTGATGCTGC 304
|||
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATTCGTTGGTTGTAC 240
|||
Db 305 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATTCGTTGGTTGTAC 364
|||
QY 241 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTATCCATCCCA 300
|||
Db 365 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTATCCATCCCA 424
|||
QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
|||
Db 425 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484
|||
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
|||
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544
|||
QY 421 GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCCTGGTGAAAAATATCCACTTTGTGT 480
|||
Db 545 GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCCTGGTGAAAAATATCCACTTTGTGT 604
|||
QY 481 TTTTCTCATGCTTGGGGCAATTCAGGACACCTTATTTCTGCTATTGGCATTTGACCTGGC 540
|||
Db 605 TTTTCTCATGCTTGGGGCAATTCAGGACACCTTATTTCTGCTATTGGCATTTGACCTGGC 664
|||
QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTTCACTTA 600
|||
Db 665 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTTCACTTA 724
|||
QY 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 660
|||
Db 725 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 784
|||
QY 661 CCTGAAACAAGAGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGA 720
|||
Db 785 CCTGAAACAAGAGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGA 844
|||
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGACATGATGGAAGCCAGTGAAGATGC 780
|||
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGACATGATGGAAGCCAGTGAAGATGC 904
|||
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGACTCTATTGATAGGGAAAAATAGC 840
|||
Db 905 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGACTCTATTGATAGGGAAAAATAGC 964
|||
QY 841 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
|||
Db 965 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
|||
QY 901 ATTGAGATGTGGTATGCTCCCTGGATGCTGATGTTTCCACTGGGTGATGAAGTATATTC 960
|||
Db 1025 ATTGAGATGTGGTATGCTCCCTGGATGCTGATGTTTCCACTGGGTGATGAAGTATATTC 1084
|||
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1020
|||
Db 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1144
|||
QY 1021 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
|||
Db 1145 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1204
|||
QY 1081 TTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCAACTGGCAAAATATTTGGACACAT 1140
|||
Db 1205 TTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCAACTGGCAAAATATTTGGACACAT 1264
|||

Qy 1141 GCTCAAAATTAAAGGGAGACATAGATTCAATGCGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1265 GCTCAAAATTAAAGGGAGACATAGATTCAATGCTAGCTATTGATCTTAGCAACAAAGCTTC 1324
Qy 1201 ATTAGCAATCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCAATCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384
Qy 1261 GATTGAAGGAGATGATGAGAATCTTATTCAGGGGACCAACATTAAACACACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAATCTTATTCAGGGGACCAACATTAAACACACCAATCAACA 1444
Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 13

ADP23966
ID ADP23966 standard; cDNA; 1505 BP.
XX
AC ADP23966;
XX
DT 18-NOV-2004 (first entry)
DE PRO polypeptide encoding cDNA SEQ ID NO:1144.
XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.
XX Unidentified.

PN WO2004041170-A2.

XX 21-MAY-2004.

PF 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;

XX WPI; 2004-419628/39.
DR P-PSDB; ADP23967.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.

XX Claim 1; SEQ ID NO 1144; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,

CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence encodes a PRO protein of
CC the invention.

XX
SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.9%; Score 1359.4; DB 13; Length 1505;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTCCACCAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTCCACCAATTCATGT 184
Qy 61 GCTTTTCTGCCTCTGCGGCTGCCTGGCTGTGTTTATCTCTTTGACTGGCAATACATAA 120
Db 185 GCTTTTCTGCCTCTGCGGCTGCCTGGCTGTGTTTATCTCTTTGACTGGCAATACATAA 244
Qy 121 TCCTGTGCCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
Db 245 TCCTGTGCCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 304
Qy 181 TGCAAGCTTTGGCCAAACTAAATCCCGCGGGGAAATGGGCTTATTCGTTGGTTGTAC 240
Db 305 TGCAAGCTTTGGCCAAACTAAATCCCGCGGGGAAATGGGCTTATTCGTTGGTTGTAC 364
Qy 241 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTGCGGTTTATATATCCATCCCA 300
Db 365 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTGCGGTTTATATATCCATCCCA 424
Qy 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATATTTTGGGGTCTTAG 484
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTGGTTCAAT 544
Qy 421 GACAACTCCTGCAAACTGGAATTCCTCTCTGAGGCTGGTGAATAATFCCACTTGTGT 480
Db 545 GACAACTCCTGCAAACTGGAATTCCTCTCTGAGGCTGGTGAATAATFCCACTTGTGT 604
Qy 481 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTTATCTGCTATTGGCATTGACCTGGC 540
Db 605 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTTATCTGCTATTGGCATTGACCTGGC 664
Qy 541 ATCTCATGGGTTTATAGTTGCTGCTGAGAAACACAGAGATAGATCTGCAACTTA 600
Db 665 ATCTCATGGGTTTATAGTTGCTGCTGAGAAACACAGAGATAGATCTGCAACTTA 724
Qy 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 784
Qy 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 785 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 844
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATGGAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATGGAAGCCAGTGAAGATGC 904
Qy 781 ATTAGATTTAAAGTTTGTATATGGAACACTGAAGGACTCTATTGATAGGAAAAAATAGC 840

Db 905 ATTAGATTAAAGTTTGATATGGAACAACAACTGAAGGACTCTATTGATAGGGAAAAATAGC 964

Qy 841 AGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTACAGACTCTTTAGTGAAGATCAGAG 900

Db 965 AGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTACAGACTCTTTAGTGAAGATCAGAG 1024

Qy 901 ATTACAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960

Db 1025 ATTACAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084

Qy 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1020

Db 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1144

Qy 1021 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080

Db 1145 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1204

Qy 1081 TTCAGTCCACCAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140

Db 1205 TTCAGTCCACCAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1264

Qy 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAAGCTTC 1200

Db 1265 GCTCAAAATTAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTTAGCAACAAAGCTTC 1324

Qy 1201 ATTAGCATCTTACAAAAGCATTTTAGGACTTCATAAAGATTTTGTGATCAGTGGGACTGTT 1260

Db 1325 ATTAGCATCTTACAAAAGCATTTTAGGACTTCATAAAGATTTTGTGATCAGTGGGACTGTT 1384

Qy 1261 GATTGAAGGAGATGATGAGAAATCTTTATTCAGGGACCAACATTAAACCAACCAATCAACA 1320

Db 1385 GATTGAAGGAGATGATGAGAAATCTTTATTCAGGGACCAACATTAAACCAACCAATCAACA 1444

Qy 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361

Db 1445 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1485

RESULT 14

AAQ87947

ID AAQ87947 standard; cDNA; 1520 BP.

XX AAQ87947;

AC AAQ87947;

XX 25-MAR-2003 (revised)

DT 06-DEC-1995 (first entry)

XX Human platelet activating factor, acetyl hydrolase (PAF-AH), cDNA.

DE Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

XX disease; pleurisy; diagnosis, ss.

OS Homo sapiens.

XX Key Location/Qualifiers

PH 162..1487

FT /*tag= a

FT /product= "Acetyl_hydrolase."

XX WO9509921-A1.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US011340.

XX 06-OCT-1993; 93US-00133803.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

PI Wilder CL;

XX

DR WPI; 1995-155262/20.

DR P-PSDB; AAR71913.

XX

PT New nucleic acid encoding platelet activating factor, acetyl:hydrolase -

PT useful in diagnosis and for treating inflammatory diseases, e.g.

PT pleurisy.

XX

PS Claim 4; Page 51-53; 88pp; English.

XX

CC The human acetyl hydrolase gene (AAQ87947) has been isolated and

CC purified. The platelet activating factor acetyl hydrolase (AAR71913) is

CC useful in the treatment of inflammatory diseases, in particular pleurisy,

CC asthma, rhinitis and eczema. The gene may also be used in raising

CC monoclonal antibodies specific for PAF-AH that are useful in the

CC diagnosis of such diseases. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.9%; Score 1359.4; DB 2; Length 1520;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTCATGT 60

Db 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTCATGT 184

Qy 61 GCCTTTCTGCCTCTGCGGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Db 185 GCCTTTCTGCCTCTGCGGCTGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244

Qy 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAATACAGTACTGATGCTGC 180

Db 245 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAATACAGTACTGATGCTGC 304

Qy 181 TGCAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCTTATTCCTGCTGCTGCTGCTGCT 240

Db 305 TGCAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCTTATTCCTGCTGCTGCTGCTGCT 364

Qy 241 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTCTTGGCTTATATATATATATATATAT 300

Db 365 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTCTTGGCTTATATATATATATATATAT 424

Qy 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360

Db 425 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484

Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420

Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544

Qy 421 GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT 480

Db 545 GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT 604

Qy 481 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATTTCTGCTATTGGCATTGACCTGGC 540

Db 605 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATTTCTGCTATTGGCATTGACCTGGC 664

Qy 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACACAGATAGATCTGCAACTTA 600

Db 665 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACACAGATAGATCTGCAACTTA 724

Qy 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660

Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 784

Qy 661 CCTGAAACAAGAGGAGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGA 720

Db 785 CCTGAAACAAGAGGAGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGA 844

Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTCATGGAAGCCAGTGAAGATGC 780

Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTCATGGAAGCCAGTGAAGATGC 904

QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAAAAAATAGC 840
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
905 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAAAAAATAGC 964
QY 841 AGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
965 AGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
QY 901 ATTCAGATGTGTATTGCCCTGGATGTCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1025 ATTCAGATGTGTATTGCCCTGGATGTCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
QY 961 CAGAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTCTGCTAATAT 1020
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1085 CAGAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTCTGCTAATAT 1144
QY 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1145 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1204
QY 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACCTTTTGCAACTGGCAAAATATTTGGACACAT 1140
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1205 TTCAGTCCACCAGAAATTTTGTGACTTCACCTTTTGCAACTGGCAAAATATTTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAAGCTTC 1200
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1265 GCTCAAAATTAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTTAGCAACAAAGCTTC 1324
QY 1201 ATTAGCATTTCTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1325 ATTAGCATTTCTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGATCTTTATTCAGGGACCAACATTAAACAAACCAATCAACA 1320
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1385 GATTGAAGGAGATGATGAGATCTTTATTCAGGGACCAACATTAAACAAACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 15
AAT80564
ID AAT80564 standard; cDNA; 1520 BP.
XX
AC AAT80564;
XX
DT 25-MAR-2003 (revised)
DT 04-NOV-1997 (first entry)
XX
DE Human plasma platelet activating factor acetylhydrolase encoding cDNA.
XX
KW Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;
KW pro-inflammatory arachidonic acid metabolite; reperfusion injury;
KW central nervous system shock; arthritis; Crohn's disease;
KW systemic lupus erythematosus; adult respiratory distress syndrome; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 162..1487
FT /*tag= a
FT /product= "PAF-AH"
XX
XX US5641669-A.
PN
XX 24-JUN-1997.
XX
XX 06-OCT-1994; 94US-00318905.
PF
XX 06-OCT-1993; 93US-00133803.
PR
XX

(ICOS-) ICOS CORP.
PA Tjoelker LM, Trong HL, Cousens LS, Wilder CL, Eberhardt CD;
XX Gray P;
PI
PI
XX
DR WPI; 1997-340947/31.
DR P-PSDB; AAW23796.
XX
PT New human plasma platelet activating factor acetylhydrolase - useful as
XX anti-inflammatory for treatment of asthma, anaphylaxis, shock, etc.
PS Example 3; Col 35-38; 43pp; English.
XX
CC The present sequence encodes the purified and isolated human plasma
CC platelet activating factor acetylhydrolase (PAF-AH). This novel
CC polypeptide inactivates PAF and oxidatively fragmented phospholipids such
CC as pro-inflammatory arachidonic acid metabolites, and so can be used to
CC treat inflammation by augmenting endogenous activity. Typical
CC applications are in asthma, anaphylaxis, shock, reperfusion injury,
CC central nervous system shock, arthritis, Crohn's disease, systemic lupus
CC erythematosus, adult respiratory distress syndrome. The polypeptide can
CC also be used to raise specific antibodies (Ab) which are useful as
CC immunoassay reagents and for generating anti-idiotypic antibodies. The
CC nucleic acid (present sequence) can be used to screen for related genes;
CC in hybridisation assays to assess the protein-producing cells; to
CC generate knockout mice; to detect genetic mutations and (antisense
CC sequences) to inhibit the protein expression. Unlike PAF receptor
CC antagonists, the protein is a natural component of plasma. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX
SQ Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 U; 0 Other;
Query Match 99.9%; Score 1359.4; DB 2; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 184
QY 61 GCTTTTCTGCTCTGCGGCTGCCCTGGCTGCTGCTTTATCCTTTTGACTGGCAATACATAA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
185 GCTTTTCTGCTCTGCGGCTGCCCTGGCTGCTGCTTTATCCTTTTGACTGGCAATACATAA 244
QY 121 TCCTGTTGCCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
245 TCCTGTTGCCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGCCCTTATTCGTTGGTTGTAC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
305 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGCCCTTATTCGTTGGTTGTAC 364
QY 241 AGACTTAATGTTTGTATCACAATAAGGGCACCTTCTTGGCGTTTATATATCCATCCCA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
365 AGACTTAATGTTTGTATCACAATAAGGGCACCTTCTTGGCGTTTATATATCCATCCCA 424
QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATATTTTGGGGTCTTAG 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
425 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATATTTTGGGGTCTTAG 484
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544
QY 421 GACAACTCCTGCAAACTGGAAATTCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
545 GACAACTCCTGCAAACTGGAAATTCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT 604
QY 481 TTTTCTCATGGTCTTTGGGGCATTTCAGGACACTTTTATCTGCTATTGGCAATTGACCTGGC 540
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
605 TTTTCTCATGGTCTTTGGGGCATTTCAGGACACTTTTATCTGCTATTGGCAATTGACCTGGC 664
QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCAATCTGCAACTTA 600

Db	665	ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA	724
Qy	601	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAAAGTCTTGGCTCTACCTTAGAAC	660
Db	725	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAAAGTCTTGGCTCTACCTTAGAAC	784
Qy	661	CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA	720
Db	785	CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA	844
Qy	721	ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATCATGGAAAGCCAGTGAAGAATGC	780
Db	845	ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGATCATGGAAAGCCAGTGAAGAATGC	904
Qy	781	ATTAGATTTAAAGTTTGATATGGAAACAACCTGAAGGACTCTATTGATAGGAAAAAATAGC	840
Db	905	ATTAGATTTAAAGTTTGATATGGAAACAACCTGAAGGACTCTATTGATAGGAAAAAATAGC	964
Qy	841	AGTAATTGGACATTCTTTTGGTGGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG	900
Db	965	AGTAATTGGACATTCTTTTGGTGGAGCAACCGTTATTTCAGACTCTTAGTGAAGATCAGAG	1024
Qy	901	ATTCAGATGTGGTATTGCCCTGGATGCAATGGATGTTTCCACTGGGTGATGAAGTATATTC	960
Db	1025	ATTCAGATGTGGTATTGCCCTGGATGCAATGGATGTTTCCACTGGGTGATGAAGTATATTC	1084
Qy	961	CAGAAATCTCAGCCCCCTCTTTTATCAACTCTGAAATATTTCCAATATCCTGCTAATAT	1020
Db	1085	CAGAAATCTCAGCCCCCTCTTTTATCAACTCTGAAATATTTCCAATATCCTGCTAATAT	1144
Qy	1021	CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG	1080
Db	1145	CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG	1204
Qy	1081	TTCAAGTCCACCAAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAAATAATGGACACAT	1140
Db	1205	TTCAAGTCCACCAAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAAATAATGGACACAT	1264
Qy	1141	GCTCAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC	1200
Db	1265	GCTCAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC	1324
Qy	1201	ATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT	1260
Db	1325	ATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT	1384
Qy	1261	GATTGAAGGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAAACCAATCAACA	1320
Db	1385	GATTGAAGGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAAACCAATCAACA	1444
Qy	1321	CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT	1361
Db	1445	CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT	1485

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:21 ; Search time 274.378 Seconds
(without alignments)
8116.452 Million cell updates/sec

Title: US-09-922-067F-9
Perfect score: 1361
Sequence: 1 tgagagactaagctgaaact.....aggaatagagaaatacaatt 1361

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1361	100.0	1361	2	US-08-557-892-9 Sequence 9, Appli
2	1361	100.0	1361	2	US-08-387-858A-9 Sequence 9, Appli
3	1361	100.0	1361	3	US-09-294-384B-9 Sequence 9, Appli
4	1361	100.0	1361	3	US-08-717-079-9 Sequence 9, Appli
5	1359.4	99.9	1520	1	US-08-470-187-7 Sequence 7, Appli
6	1359.4	99.9	1520	1	US-08-318-905-7 Sequence 7, Appli
7	1359.4	99.9	1520	1	US-08-483-232-7 Sequence 7, Appli
8	1359.4	99.9	1520	1	US-08-483-140-7 Sequence 7, Appli
9	1359.4	99.9	1520	2	US-08-485-938A-7 Sequence 7, Appli
10	1359.4	99.9	1520	2	US-08-910-041-7 Sequence 7, Appli
11	1359.4	99.9	1520	3	US-09-328-474-7 Sequence 7, Appli
12	1359.4	99.9	1520	3	US-09-100-546-7 Sequence 7, Appli
13	1359.4	99.9	1520	3	US-09-010-715-7 Sequence 7, Appli
14	1359.4	99.9	1520	3	US-09-577-758-7 Sequence 7, Appli
15	1162.4	85.4	1335	1	US-08-483-232-30 Sequence 30, Appli
16	1162.4	85.4	1335	2	US-08-485-938A-30 Sequence 30, Appli
17	1162.4	85.4	1335	2	US-08-910-041-30 Sequence 30, Appli
18	1162.4	85.4	1335	3	US-09-328-474-30 Sequence 30, Appli
19	1162.4	85.4	1335	3	US-09-100-546-30 Sequence 30, Appli
20	1162.4	85.4	1335	3	US-09-010-715-30 Sequence 30, Appli
21	1162.4	85.4	1335	3	US-09-577-758-30 Sequence 30, Appli
22	1049.6	77.1	1533	1	US-08-483-232-23 Sequence 23, Appli
23	1049.6	77.1	1533	2	US-08-485-938A-23 Sequence 23, Appli
24	1049.6	77.1	1533	2	US-08-910-041-23 Sequence 23, Appli
25	1049.6	77.1	1533	3	US-09-328-474-23 Sequence 23, Appli
26	1049.6	77.1	1533	3	US-09-100-546-23 Sequence 23, Appli
27	1049.6	77.1	1533	3	US-09-010-715-23 Sequence 23, Appli

28	1049.6	77.1	1533	3	US-09-577-758-23 Sequence 23, Appli
29	1043.2	76.6	2191	1	US-08-318-905-22 Sequence 22, Appli
30	1043.2	76.6	2191	1	US-08-483-232-22 Sequence 22, Appli
31	1043.2	76.6	2191	1	US-08-483-140-22 Sequence 22, Appli
32	1043.2	76.6	2191	2	US-08-485-938A-22 Sequence 22, Appli
33	1043.2	76.6	2191	2	US-08-910-041-22 Sequence 22, Appli
34	1043.2	76.6	2191	3	US-09-328-474-22 Sequence 22, Appli
35	1043.2	76.6	2191	3	US-09-100-546-22 Sequence 22, Appli
36	1043.2	76.6	2191	3	US-09-010-715-22 Sequence 22, Appli
37	1043.2	76.6	2191	3	US-09-577-758-22 Sequence 22, Appli
38	783.6	57.6	1494	1	US-08-318-905-21 Sequence 21, Appli
39	783.6	57.6	1494	1	US-08-483-232-21 Sequence 21, Appli
40	783.6	57.6	1494	1	US-08-483-140-21 Sequence 21, Appli
41	783.6	57.6	1494	2	US-08-485-938A-21 Sequence 21, Appli
42	783.6	57.6	1494	2	US-08-910-041-21 Sequence 21, Appli
43	783.6	57.6	1494	3	US-09-328-474-21 Sequence 21, Appli
44	783.6	57.6	1494	3	US-09-100-546-21 Sequence 21, Appli
45	783.6	57.6	1494	3	US-09-010-715-21 Sequence 21, Appli

ALIGNMENTS

RESULT 1
US-08-557-892-9
; Sequence 9, Application US/08557892
; Patent No. 5968818
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,892
; FILING DATE: 14 No. 5968818ember 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,858
; FILING DATE: 14 No. 5968818ember 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,187

```
Query Match      99.9%; Score 1359.4; DB 1; Length 1520;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0;
```

Qy	1	184	60	120	180	240	300	360	420	480	540	600	660	724
Db	125	184	60	120	180	240	300	360	420	480	540	600	664	724
Qy	61	120	180	240	300	360	420	480	544	604	664	724	784	848
Db	185	244	304	364	424	484	544	604	664	724	784	848	912	976
Qy	121	180	240	300	360	420	480	540	600	660	720	780	840	900
Db	245	304	364	424	484	544	604	664	724	784	844	904	964	1024
Qy	181	240	300	360	420	480	540	600	660	720	780	840	900	960
Db	305	364	424	484	544	604	664	724	784	844	904	964	1024	1084
Qy	241	300	360	420	480	540	600	660	720	780	840	900	960	1020
Db	365	424	484	544	604	664	724	784	844	904	964	1024	1084	1144
Qy	301	360	420	480	540	600	660	720	780	840	900	960	1020	1080
Db	425	484	544	604	664	724	784	844	904	964	1024	1084	1144	1204
Qy	361	420	480	540	600	660	720	780	840	900	960	1020	1080	1140
Db	485	544	604	664	724	784	844	904	964	1024	1084	1144	1204	1264
Qy	421	480	540	600	660	720	780	840	900	960	1020	1080	1140	1200
Db	545	604	664	724	784	844	904	964	1024	1084	1144	1204	1264	1324
Qy	481	540	600	660	720	780	840	900	960	1020	1080	1140	1200	1260
Db	605	664	724	784	844	904	964	1024	1084	1144	1204	1264	1324	1384
Qy	541	600	660	720	780	840	900	960	1020	1080	1140	1200	1260	1320
Db	665	724	784	844	904	964	1024	1084	1144	1204	1264	1324	1384	1444

QY	601	CTATTTCAAGGACCAATCTGCTGCAGAAATPAGGGACAAAGTCTTGGCTCTACCTTAGAAC	660
DB	725	CTATTTCAAGGACCAATCTGCTGCAGAAATPAGGGACAAAGTCTTGGCTCTACCTTAGAAC	784
QY	661	CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAAAGAGCAAAAAGA	720
DB	785	CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAAAGAGCAAAAAGA	844
QY	721	ATGTTCCCAAGCTCTCAGTCTGATTCCTTGACATTTGATCATGGAAGCCAGTGAAGAAATGC	780
DB	845	ATGTTCCCAAGCTCTCAGTCTGATTCCTTGACATTTGATCATGGAAGCCAGTGAAGAAATGC	904
QY	781	ATTAGATTTAAAGTTTGATATGGAAACAACCTGAAGGACTTATTTGATAGGAAAAAATAGC	840
DB	905	ATTAGATTTAAAGTTTGATATGGAAACAACCTGAAGGACTTATTTGATAGGAAAAAATAGC	964
QY	841	AGTAAATTGGACATTCCTTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG	900
DB	965	AGTAAATTGGACATTCCTTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG	1024
QY	901	ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC	960
DB	1025	ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC	1084
QY	961	CAGAAATTCCTCAGCCCCCTCTTTTTTATCRAACTCTGAATATTTCCAATATCTCTGCTAATAT	1020
DB	1085	CAGAAATTCCTCAGCCCCCTCTTTTTTATCRAACTCTGAATATTTCCAATATCTCTGCTAATAT	1144
QY	1021	CATAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG	1080
DB	1145	CATAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG	1204
QY	1081	TTCAGTCCACCAGAAATTTTGTCTGACTTCACCTTTTGCACTGGCAAAATAATTTGGACACAT	1140
DB	1205	TTCAGTCCACCAGAAATTTTGTCTGACTTCACCTTTTGCACTGGCAAAATAATTTGGACACAT	1264
QY	1141	GCTCAAAATTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAGCTTC	1200
DB	1265	GCTCAAAATTAAGGGGAGACATAGATTCAAATGTAGCTATTGATCTTTAGCAACAAGCTTC	1324
QY	1201	ATTAGCAATTTTACAAAAGCATTTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT	1260
DB	1325	ATTAGCAATTTTACAAAAGCATTTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT	1384
QY	1261	GATTGAAGGAGATGATGAGAAATCTTATTCCAGGGACCAACATTAACACAACCAATCAACA	1320
DB	1385	GATTGAAGGAGATGATGAGAAATCTTATTCCAGGGACCAACATTAACACAACCAATCAACA	1444
QY	1321	CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT	1361
DB	1445	CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT	1485

RESULT 6
US-08-318-905-7
; Sequence 7, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois


```

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
;
; US-08-483-232-7

```

	Query Match	99.9%;	Score 1359.4;	DB 1;	Length 1520;
	Best Local Similarity	99.9%;	Pred. No. 0;		
	Matches 1360;	Conservative	0; Mismatches	1; Indels	0; Gaps
Qy	1	TGAGAGACTAAGCTGAAC	TGCTGCTCAGCTCCCAAGATGGTGCACCACCAAAATTGCATGT	60	
Dd	125	TGAGAGACTAAGCTGAAC	TGCTGCTCAGCTCCCAAGATGGTGCACCACCAAAATTGCATGT	184	
Qy	61	GCTTTTCTGCTCTCGGCTGCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATAAA	120		
Dd	185	GCTTTTCTGCTCTCGGCTGCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATAAA	244		
Qy	121	TCCTGTTGCCCATATGAAATCATCAGCATGGTCAACAAAATACAAGTACTGATGGCTGC	180		
Dd	245	TCCTGTTGCCCATATGAAATCATCAGCATGGTCAACAAAATACAAGTACTGATGGCTGC	304		
Qy	181	TGCAAGCTTTGGCCAAA	CTAAAAATCCCCCGGGGAAATGGGCCCTTATTCCGTTGGTTGTAC	240	
Dd	305	TGCAAGCTTTGGCCAAA	CTAAAAATCCCCCGGGGAAATGGGCCCTTATTCCGTTGGTTGTAC	364	
Qy	241	AGACTTAATGTTTGATCACACTAATAAGGGACCTTCTTGGCGTTTATATTATCCATCCCCA	300		
Dd	365	AGACTTAATGTTTGATCACACTAATAAGGGACCTTCTTGGCGTTTATATTATCCATCCCCA	424		
Qy	301	AGATAATGATCGCCTTGACACCCCTTTGGATCCCAAATAAAGAATATTTTTGGGGTCTTAG	360		
Dd	425	AGATAATGATCGCCTTGACACCCCTTTGGATCCCAAATAAAGAATATTTTTGGGGTCTTAG	484		
Qy	361	CAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT	420		
Dd	485	CAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT	544		

QY	421	GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT	480
Db	545	GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT	604
QY	481	TTTTTCTCATGGTCTTTGGGCATTTCAGGACACTTTTATCTGTCTATTGGCATTTGACCTGGC	540
Db	605	TTTTTCTCATGGTCTTTGGGCATTTCAGGACACTTTTATCTGTCTATTGGCATTTGACCTGGC	664
QY	541	ATCTCATGGGTTTATAGTTGCTGTCTGTAGAAACACAGAGATAGATCTGCATCTGCAACTTA	600
Db	665	ATCTCATGGGTTTATAGTTGCTGTCTGTAGAAACACAGAGATAGATCTGCATCTGCAACTTA	724
QY	601	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAGTCTTGGCTCTACCTTAGAAC	660
Db	725	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAGTCTTGGCTCTACCTTAGAAC	784
QY	661	CCTGAAACAAAGAGGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA	720
Db	785	CCTGAAACAAAGAGGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA	844
QY	721	ATGTTCCCAAGCTCTCAGTCTGATTCCTTGACATTTGATCATGGAAAGCCAGTGAAGATGC	780
Db	845	ATGTTCCCAAGCTCTCAGTCTGATTCCTTGACATTTGATCATGGAAAGCCAGTGAAGATGC	904
QY	781	ATTAGATTTAAAGTTTGATATGGAACTGAAGGACTCTATTGATAGGGAAAAAATAGC	840
Db	905	ATTAGATTTAAAGTTTGATATGGAACTGAAGGACTCTATTGATAGGGAAAAAATAGC	964
QY	841	AGTAATTGGACATTCCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG	900
Db	965	AGTAATTGGACATTCCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG	1024
QY	901	ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTTCCACTGGGTGATGAAGTATATTC	960
Db	1025	ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTTCCACTGGGTGATGAAGTATATTC	1084
QY	961	CAGAAATTCCTCAGCCCCCTTTTTTTTATCAACTCTGAATATTTTCCAAATATCCTGCTAATAT	1020
Db	1085	CAGAAATTCCTCAGCCCCCTTTTTTTTATCAACTCTGAATATTTTCCAAATATCCTGCTAATAT	1144
QY	1021	CATAAAATGAAAAAATGCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGG	1080
Db	1145	CATAAAATGAAAAAATGCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGG	1204
QY	1081	TTCAGTCCACAGAAATTTTGCTGACTTCACCTTTTGCAACTGGCAAAATAAATGGACACAT	1140
Db	1205	TTCAGTCCACAGAAATTTTGCTGACTTCACCTTTTGCAACTGGCAAAATAAATGGACACAT	1264
QY	1141	GCTCAAAATTAAGGGGAGACATAGATTCAAATGCAGCTAATTGATCTTAGCAACAAAAGCTTC	1200
Db	1265	GCTCAAAATTAAGGGGAGACATAGATTCAAATGTAGCTAATTGATCTTAGCAACAAAAGCTTC	1324
QY	1201	ATTAGCATTTCTACAAAAGCATTTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT	1260
Db	1325	ATTAGCATTTCTACAAAAGCATTTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT	1384
QY	1261	GATTGAAGGAGATGATGAGAAATCTTATTCCAGGGACCAACATTAACACAACTCAATCAACA	1320
Db	1385	GATTGAAGGAGATGATGAGAAATCTTATTCCAGGGACCAACATTAACACAACTCAATCAACA	1444
QY	1321	CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT	1361
Db	1445	CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT	1485

RESULT 8
US-08-483-140-7
; Sequence 7, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase

NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/483,140
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
US-08-483-140-7

Query Match 99.9%; Score 1359.4; DB 1; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAATTGCATGT 60
DB 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAATTGCATGT 184
QY 61 GCTTTTCTGCTCTGCGGCTGCCTGGCTGGTGTATCCCTTTGACTGGCAATACATAAA 120
DB 185 GCTTTTCTGCTCTGCGGCTGCCTGGCTGGTGTATCCCTTTGACTGGCAATACATAAA 244
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAGTACTGATGGCTGC 180
DB 245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAGTACTGATGGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTAAATAATCCCGGGGAAATGGGCTTATCCCTGGTGTATC 240
DB 305 TGCAAGCTTTGGCCAAACTAAATAATCCCGGGGAAATGGGCTTATCCCTGGTGTATC 364
QY 241 AGACTTAATGTTGATCACAATAAAGGCACCTTCTTGGGTTTATATATCCATCCCA 300
DB 365 AGACTTAATGTTGATCACAATAAAGGCACCTTCTTGGGTTTATATATCCATCCCA 424
QY 301 AGATAATGATCGCCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGCTTTAG 360
DB 425 AGATAATGATCGCCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGCTTTAG 484
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTTCAGGTTTACTCTTTGGTTCAAT 420

DB 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTTCAGGTTACTCTTTGGTTCAAT 544
QY 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAAAAATATCCACTTGTGT 480
DB 545 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAAAAATATCCACTTGTGT 604
QY 481 TTTTCTCATGGTCTTGGGGCATTTCAGGACACTTTTATCTGCTATTGGCAATTGACCTGGC 540
DB 605 TTTTCTCATGGTCTTGGGGCATTTCAGGACACTTTTATCTGCTATTGGCAATTGACCTGGC 664
QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
DB 665 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 660
DB 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTACCTTAGAAC 784
QY 661 CCTGAACAAGAGAGGAGAGACACATATACGAAATGAGCAGTACGGCAAGAGCAAAAGA 720
DB 785 CCTGAACAAGAGAGGAGAGACACATATACGAAATGAGCAGTACGGCAAGAGCAAAAGA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
DB 845 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 904
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACTGGAAGGACTCTATTGATAGGGAATAATAGC 840
DB 905 ATTAGATTTAAAGTTTGATATGGAACAACTGGAAGGACTCTATTGATAGGGAATAATAGC 964
QY 841 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
DB 965 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
QY 901 ATTGAGATGTTGGTATTGCCCTGGATGATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
DB 1025 ATTGAGATGTTGGTATTGCCCTGGATGATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTAATAT 1020
DB 1085 CAGAAATCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTAATAT 1144
QY 1021 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
DB 1145 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1204
QY 1081 TTCAGTCCACAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACAT 1140
DB 1205 TTCAGTCCACAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAATGCAAGTATTGATCTTAGCAAAAAGCTTC 1200
DB 1265 GCTCAAAATTAAGGGAGACATAGATTCAATGCTAGCTATTGATCTTAGCAAAAAGCTTC 1324
QY 1201 ATTAGCAATTTTACAAAAGCAATTTAGGACTTCAATAAGATTTTATGATCAGTGGGACTGCTT 1260
DB 1325 ATTAGCAATTTTACAAAAGCAATTTAGGACTTCAATAAGATTTTATGATCAGTGGGACTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGAATCTTATCCAGGGACCAACATTAACACCAACCAATCAACA 1320
DB 1385 GATTGAAGGAGATGATGAGAATCTTATCCAGGGACCAACATTAACACCAACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAT 1361
DB 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAT 1485

RESULT 9
US-08-485-938A-7
; Sequence 7, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.


```

RESULT 10
US-08-910-041-7
; Sequence 7, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
;
US-08-910-041-7

```

	Query Match	99.9%;	Score 1359.4;	DB 2;	Length 1520;
	Best Local Similarity	99.9%;	Pred. NO. 0;		
	Matches 1360;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
Qy	1	TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGGCCACCCAAATTGCATGT	60		
Db	125	TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGGCCACCCAAATTGCATGT	184		
Qy	61	GCTTTTCTGCCTCTCGGGCTGCCTGGCTGTGGTTTATCCTTTTGTACTGGCAATACATAAA	120		
Db	185	GCTTTTCTGCCTCTCGGGCTGCCTGGCTGTGGTTTATCCTTTTGTACTGGCAATACATAAA	244		
Qy	121	TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGC	180		

Db	245	TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAGTACTGATGGCTGC	304
Qy	181	TGCAAGCTTTTGGCCAAACTAAAAATCCCCGGGGAAAATGGGCCCTTATTCGGTTGGTTGTAC	240
Db	305	TGCAAGCTTTTGGCCAAACTAAAAATCCCCGGGGAAAATGGGCCCTTATTCGGTTGGTTGTAC	364
Qy	241	AGACTTAATGTTTGATCACACATAAAGGSCACCTTCTTGCGTTTATATTATCCATFCCCA	300
Db	365	AGACTTAATGTTTGATCACACATAAAGGSCACCTTCTTGCGTTTATATTATCCATFCCCA	424
Qy	301	AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGCTTTAG	360
Db	425	AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGCTTTAG	484
Qy	361	CAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT	420
Db	485	CAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT	544
Qy	421	GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCCCTGGTGAAAAATATCCAATTGTTGT	480
Db	545	GACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCCCTGGTGAAAAATATCCAATTGTTGT	604
Qy	481	TTTTTCTCATGGTCTTGGGGCATTCAGGACACTTTTATTTCTGCTATTGGCATTTGACCTGGC	540
Db	605	TTTTTCTCATGGTCTTGGGGCATTCAGGACACTTTTATTTCTGCTATTGGCATTTGACCTGGC	664
Qy	541	ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA	600
Db	665	ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA	724
Qy	601	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAGTCTTGGCTCTACCTTAGAATC	660
Db	725	CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAGTCTTGGCTCTACCTTAGAATC	784
Qy	661	CCTGAAAAAAGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA	720
Db	785	CCTGAAAAAAGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA	844
Qy	721	ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGTATCATGGAAGCCAGTGAAGATGC	780
Db	845	ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGTATCATGGAAGCCAGTGAAGATGC	904
Qy	781	ATTAGATTTAAAGTTTGATATGGAACTGAAGGACTCTATTGTATAGGAAAAAATAGC	840
Db	905	ATTAGATTTAAAGTTTGATATGGAACTGAAGGACTCTATTGTATAGGAAAAAATAGC	964
Qy	841	AGTAATTGGACATTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG	900
Db	965	AGTAATTGGACATTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG	1024
Qy	901	ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC	960
Db	1025	ATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC	1084
Qy	961	CAGAAATTCCTCAGCCCTCTTTTTTTATCAACTCTGAATATTTTCCAATATCCTGCTAATAT	1020
Db	1085	CAGAAATTCCTCAGCCCTCTTTTTTTATCAACTCTGAATATTTTCCAATATCCTGCTAATAT	1144
Qy	1021	CATAAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG	1080
Db	1145	CATAAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG	1204
Qy	1081	TTCACTCCACCAGAAATTTTGCTGACTTCACCTTTTGCAACTGSCAAAAATAATTGGACACAT	1140
Db	1205	TTCACTCCACCAGAAATTTTGCTGACTTCACCTTTTGCAACTGSCAAAAATAATTGGACACAT	1264
Qy	1141	GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGTATCTTAGCAACAAGCTTC	1200
Db	1265	GCTCAAAATTAAGGGAGACATAGATTCAAATGTAGCTATTGTATCTTAGCAACAAGCTTC	1324
Qy	1201	ATTAGCATTTCTTACAAAGCATTTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTT	1260

Db 1325 ATTAGCATCTTACAAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384
Qy 1261 GATTGAAGGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAACCAATCAACA 1444
Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 11

US-09-328-474-7
; Sequence 7, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/328,474

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448

TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484

US-09-328-474-7

Query Match 99.9%; Score 1359.4; DB 3; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTGCATGT 60
Db 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTGCATGT 184
Qy 61 GCTTTTCTGCCTCTGCGGCTGCCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATAAA 120
Db 185 GCTTTTCTGCCTCTGCGGCTGCCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATAAA 244
Qy 121 TCCTGTGCCCCATATGAAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180
Db 245 TCCTGTGCCCCATATGAAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 304
Qy 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATTCGGTTGGTTGTAC 240
Db 305 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATTCGGTTGGTTGTAC 364
Qy 241 AGACTTAATGTTTGTATCACAATAAAGGGCACCTTCTTGGCTTATATATATCCATCCCA 300
Db 365 AGACTTAATGTTTGTATCACAATAAAGGGCACCTTCTTGGCTTATATATATCCATCCCA 424
Qy 301 AGATAATGATCGCTTGACACCCCTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCTTGACACCCCTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 544
Qy 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT 480
Db 545 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCTGGTGAAAAATATCCACTTGTGT 604
Qy 481 TTTTCTCATGCTTGGGGCAATTCAGGACACTTTTATCTGCTATTGGCATTTGACCTGGC 540
Db 605 TTTTCTCATGCTTGGGGCAATTCAGGACACTTTTATCTGCTATTGGCATTTGACCTGGC 664
Qy 541 ATCTCATGGGTTTATAGTTGCTGTGAGAAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db 665 ATCTCATGGGTTTATAGTTGCTGTGAGAAACACAGAGATAGATCTGCATCTGCAACTTA 724
Qy 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGCAAGTCTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGCAAGTCTTGGCTCTACCTTAGAAC 784
Qy 661 CCTGAAACAAGAGAGGAGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 785 CCTGAAACAAGAGAGGAGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 844
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTTGATGATGAAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTTGATGATGAAAGCCAGTGAAGATGC 904
Qy 781 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGAAAAAATAGC 840
Db 905 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGAAAAAATAGC 964
Qy 841 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 965 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
Qy 901 ATTCAGATGTGTTATTCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTGTTATTCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
Qy 961 CAGAAATTCCTCAGCCCCCTCTTTTATCAAACTCTGAATATTTCCAATATCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCCCTCTTTTATCAAACTCTGAATATTTCCAATATCTGCTAATAT 1144
Qy 1021 CATAAAATGAAAAAATGCTACTCACCTGATGATAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db 1145 CATAAAATGAAAAAATGCTACTCACCTGATGATAAGAAAGAAAGATGATTACAATCAGGGG 1204

QY 1081 TTCAGTCCACGAGAAATTTTGGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1140
Db 1205 TTCAGTCCACGAGAAATTTTGGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1265 GCTCAAAATTAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTAGCAACAAAGCTTC 1324
QY 1201 ATTAGCATTTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATTTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGAACTCTTATTCAGGGACCAACATTAACACAAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAACTCTTATTCAGGGACCAACATTAACACAAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 12

US-09-100-546-7
; Sequence 7, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6099836and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
US-09-100-546-7
Query Match 99.9%; Score 1359.4; DB 3; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCATGT 184
QY 61 GCTTTTCTGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 185 GCTTTTCTGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAATACAAATACAAAT 180
Db 245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAATACAAATACAAAT 304
QY 181 TGCAAGCTTTGGCCAACTAAAATCCCCCGGGGAAATGGGCTTATTCCTGGTTGTATC 240
Db 305 TGCAAGCTTTGGCCAACTAAAATCCCCCGGGGAAATGGGCTTATTCCTGGTTGTATC 364
QY 241 AGACTTAATGTTTGATCACACTAATAAGGCACACTTCTTGGCTTTATATTCATCCCATCC 300
Db 365 AGACTTAATGTTTGATCACACTAATAAGGCACACTTCTTGGCTTTATATTCATCCCATCC 424
QY 301 AGATAATGATCGCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484
QY 361 CAAATTTCTTGAACACACTGGCTTATGGCAACACTTTTGAGGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGAACACACTGGCTTATGGCAACACTTTTGAGGTTACTCTTTGGTTCAAT 544
QY 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAATAATATCCACTTGTGT 480
Db 545 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAATAATATCCACTTGTGT 604
QY 481 TTTTCTCATGTTCTTGGGCACTTCAGGACACTTTTATCTGCTATTGGCAATGACCTGGC 540
Db 605 TTTTCTCATGTTCTTGGGCACTTCAGGACACTTTTATCTGCTATTGGCAATGACCTGGC 664
QY 541 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCTATCTGCAACTTA 600
Db 665 ATCTCATGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCTATCTGCAACTTA 724
QY 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGGACAACTTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGGACAACTTTGGCTCTACCTTAGAAC 784
QY 661 CCTGAAACAAGAGAGGAGACACATATACGAAATGAGCAGTACGGCAAGAGCAAAAGA 720
Db 785 CCTGAAACAAGAGAGGAGACACATATACGAAATGAGCAGTACGGCAAGAGCAAAAGA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTCTTTCATCATTTGATGCAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTCTTTCATCATTTGATGCAAGCCAGTGAAGATGC 904
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGGGAAAAATAGC 840
Db 905 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGGGAAAAATAGC 964
QY 841 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAGATCAGAG 900
Db 965 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAGATCAGAG 1024
QY 901 ATTCAGATGTGGTATTGCTGCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTGGTATTGCTGCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084

QY 841 AGTAATTGGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 965 AGTAATTGGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
QY 901 ATTGAGATGTTGATTTGCCCTGGATGTCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTGAGATGTTGATTTGCCCTGGATGTCATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1144
QY 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACATCAGGGG 1080
Db 1145 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACATCAGGGG 1204
QY 1081 TTCAGTCCACAGAAATTTTGTGACTTCACTTTTGCAACTTTCACCTTTTGCAACTTTGGACACAT 1140
Db 1205 TTCAGTCCACAGAAATTTTGTGACTTCACTTTTGCAACTTTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGGGAGACATAGATTCAAATGACGCTATTGATCTTTAGCAACAAAGCTTC 1200
Db 1265 GCTCAAAATTAAGGGGAGACATAGATTCAAATGATGCTATTGATCTTTAGCAACAAAGCTTC 1324
QY 1201 ATTAGCATCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGAATCTTATTCAGGGAACCAACATTAACCAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAATCTTATTCAGGGAACCAACATTAACCAACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 14

US-09-577-758-7
; Sequence 7, Application US/09577758
; Patent No. 6203790
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,758
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/010,715
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993

ATTORNEY/AGENT INFORMATION:
; NAME: No. 6203790and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
US-09-577-758-7
Query Match 99.9%; Score 1359.4; DB 3; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTGCATGT 60
Db 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTGCATGT 184
QY 61 GCTTTTCTGCCTCTCGGGCTGCCTGGCTGCTGGTTTATCCTTTTGAAGTGGCAATACATAAA 120
Db 185 GCTTTTCTGCCTCTCGGGCTGCCTGGCTGCTGGTTTATCCTTTTGAAGTGGCAATACATAAA 244
QY 121 TCCTGTTGCCATATGAAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180
Db 245 TCCTGTTGCCATATGAAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTTAAATCCCGGGGAAATGGGCCTTATTCGTTGGTTGTAC 240
Db 305 TGCAAGCTTTGGCCAAACTTAAATCCCGGGGAAATGGGCCTTATTCGTTGGTTGTAC 364
QY 241 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGGCTTATATTTATCCATCCCA 300
Db 365 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGGCTTATATTTATCCATCCCA 424
QY 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATACAAATATTTTGGGTCTTAG 360
Db 425 AGATAATGATCGCTTGACACCTTTGGATCCCAATACAAATATTTTGGGTCTTAG 484
QY 361 CAAATTTCTTGAACACACATGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGAACACACATGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 544
QY 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAAATAATCCACTTGTGT 480
Db 545 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAAATAATCCACTTGTGT 604
QY 481 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATTCGCTATTGGCATTGACCTGGC 540
Db 605 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATTCGCTATTGGCATTGACCTGGC 664
QY 541 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCACTTGAAC 600
Db 665 ATCTCATGGGTTTATAGTTGCTGTAGAACACAGAGATAGATCTGCACTTGAAC 724
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACCAAGTCTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACCAAGTCTTGGCTCTACCTTAGAAC 784
QY 661 CCTGAAACAGAGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 785 CCTGAAACAGAGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780

Db 845 ATGTTCCCAAGCTCTCAGTCTGATCTTGACATGTGATCATGGAAAGCCAGTGAAGATGC 904
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACACTGAAGGACTCTATTGATAGGGAAAAAATAGC 840
Db 905 ATTAGATTTAAAGTTTGATATGGAACAACACTGAAGGACTCTATTGATAGGGAAAAAATAGC 964
QY 841 AGTAATTGGACATCTCTTTTGGTGGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 965 AGTAATTGGACATCTCTTTTGGTGGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAG 1024
QY 901 ATTCAGATGTGGTATTGCCCCTGCATGGATGTTTCCACCTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTGGTATTGCCCCTGCATGGATGTTTCCACCTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1144
QY 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAAATCAGGGG 1080
Db 1145 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAAATCAGGGG 1204
QY 1081 TTCAGTCCACCAGAAATTTTGGTGAATTTTGCACCTTTCACACTGGCAAAATAATTGGACACAT 1140
Db 1205 TTCAGTCCACCAGAAATTTTGGTGAATTTTGCACCTTTCACACTGGCAAAATAATTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1265 GCTCAAAATTAAGGGAGACATAGATTCAAAATGTAGCTATTGATCTTAGCAACAAAGCTTC 1324
QY 1201 ATTAGCATCTTACAAAAGCAATTAGGACTTCATATAAGATTTTGTATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATCTTACAAAAGCAATTAGGACTTCATATAAGATTTTGTATCAGTGGGACTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGAATCTTATTCAGGACCAACATTAACACAAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAATCTTATTCAGGACCAACATTAACACAAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATCAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATCAATT 1485

RESULT 15
US-08-483-232-30
; Sequence 30, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-483-232-30

Query Match 85.4%; Score 1162.4; DB 1; Length 1335;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 1223; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 38 ATGGTGCCACCCAAATTGCATGTGCTTTTCTGCTCTCTGCGGTGCTGCTGGTGTGTTTAT 97
Db 1 ATGGTACCCCAAGCTGCAGTCTCTGTTTGTCTGTGTGATGTCTCGCGTCTGTTGAC 60
QY 98 CCTTTTGACTGGCAATACATAAATCCTGTGTCCTTATGTCCTATATGAATCATCAGCATGGTCAAC 157
Db 61 CCTTCGATTGGCAGTATATCAACCCCGTGGCTCACATGAAGAGCAGCGCTGGTGAAT 120
QY 158 AAAATACAAGTACTGATGCTGTGCTGCAAGCTTTGGCCAAACTAAATCCCCGGGGAAT 217
Db 121 AAGATCCAGGTCTCATGCGCGCACCAAGTTCGGTCAGACCAAGATTCTCTAGAGGCAAC 180
QY 218 GGGCCTTATTCGGTTGGTTGTACAGACTTAATGTTTGTATCACACTAAATAGGCGCACCTTC 277
Db 181 GGCCCTACAGCGTGGGTGACCGATCTGATGTTTCGACCATACCAACAAAGGAATTTT 240
QY 278 TTGCGTTTATATTATCCATCCCAAGATAATGATCGCTTTGACACCCCTTTGGATCCCAAT 337
Db 241 CTGAGACTGTACTACCCCGCAGGACACAGACAGACTGGATACTCTGTGGATCCCAAT 300
QY 338 AAAGAATAATTTTGGGTCTTAGCAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATT 397
Db 301 AAAGAATAATTTTGGGTCTTAGCAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATT 360
QY 398 TTGAGGTTACTCTTTTGGTTCAATGACAACTCTGCAAACTGGAATTTCCCTCTTGAGGCCT 457
Db 361 TTGAGGTTACTCTTTTGGTTCAATGACAACTCTGCAAACTGGAATTTCCCTCTTGAGGCCT 420
QY 458 GGTGAAAAATATCCACTTGTGTTTCTCATGGTCTTGGGGCATTCAGGACACTTTAT 517
Db 421 GGTGAAAAATATCCACTTGTGTTTCTCATGGTCTTGGGGCATTCAGGACACTTTAT 480
QY 518 TCTGCTATTGGCATTGACCTGGCATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGA 577
Db 481 TCTGCTATTGGCATTGACCTGGCATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGA 540
QY 578 GATAGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 637
Db 541 GATAGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 600
QY 638 AAGTCTTGGCTCTACCTTAGAACCCCTGAAACAAGAGGAGAGACACATATACGAATGAG 697
Db 601 AAGTCTTGGCTCTACCTTAGAACCCCTGAAACAAGAGGAGAGACACATATACGAATGAG 660
QY 698 CAGGTACGGCAAGAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGATTCTTGCACATTGAT 757

Db	661		CAGGTACGGCAAGAGCAAAAGAATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTGAT	720
Qy	758		CATGGAAAGCCAGTGAAGATGCATTAGATTTAAAGTTTGGATATGGAACTGAAGGAC	817
Db	721		CATGGAAAGCCAGTGAAGATGCATTAGATTTAAAGTTTGGATATGGAACTGAAGGAC	780
Qy	818		TCTATTGATAGCGGAAAAATAGCAGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATT	877
Db	781		TCTATTGATAGCGGAAAAATAGCAGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATT	840
Qy	878		CAGACTCTTAGTGAAGATCAGAGATTCAGATGTGGTATTTGCCCTGGATGCATGGATGTTT	937
Db	841		CAGACTCTTAGTGAAGATCAGAGATTCAGATGTGGTATTTGCCCTGGATGCATGGATGTTT	900
Qy	938		CCACTGGGTGATGAAGTATATTCCAGAAATTCCTCAGCCCCCTCTTTTTTATCAACTCTGAA	997
Db	901		CCACTGGGTGATGAAGTATATTCCAGAAATTCCTCAGCCCCCTCTTTTTTATCAACTCTGAA	960
Qy	998		TATTTCCAATATCTCTGCTAATATCATAAAAATGAAAAATGCTACTCACCTGATAAAGAA	1057
Db	961		TATTTCCAATATCTCTGCTAATATCATAAAAATGAAAAATGCTACTCACCTGATAAAGAA	1020
Qy	1058		AGAAAGATGATTAAATCAGGGGTTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCA	1117
Db	1021		AGAAAGATGATTAAATCAGGGGTTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCA	1080
Qy	1118		ACTGGCAAAATAATTGGACACATGCTCAAATTAAGGGAGACATAGATTCAAATGCACT	1177
Db	1081		ACTGGCAAAATAATTGGACACATGCTCAAATTAAGGGAGACATAGATTCAAATGCACT	1140
Qy	1178		ATTGATCTTAGCAACAAAGCTTCATTAGCATTTCTACAAAGCATTTTAGGACTTTCATAAA	1237
Db	1141		ATTGATCTTAGCAACAAAGCTTCATTAGCATTTCTACAAAGCATTTTAGGACTTTCATAAA	1200
Qy	1238		GATTTTGATCAGTGGGACTGCTTGATTGAAGGAGATGATGAGAAATCTTATTTCCAGGGACC	1297
Db	1201		GATTTTGATCAGTGGGACTGCTTGATTGAAGGAGATGATGAGAAATCTTATTTCCAGGGACC	1260
Qy	1298		AACATTAAACAAACCAATCAACATCATGTTACAGAACTCTTTCAGGAATAGAGAAATAC	1357
Db	1261		AACATTAAACAAACCAATCAACATCATGTTACAGAACTCTTTCAGGAATAGAGAAATAC	1320
Qy	1358	AATT	1361	
Db	1321	AATT	1324	

Search completed: March 15, 2005, 16:15:17
Job time : 276.378 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 16:15:21 ; Search time 1326.88 Seconds
(without alignments)
6106.287 Million cell updates/sec

Title: US-09-922-067F-9
Perfect score: 1361
Sequence: 1 tgagagactaagctgaaact.....aggaatagagaatacaatt 1361

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues 11089632

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1361	100.0	1361	9	US-09-922-067-9
2	1361	100.0	1361	15	US-10-173-233-9
3	1361	100.0	1361	16	US-10-406-156-9
4	1361	100.0	1561	9	US-09-962-832-110
5	1359.4	99.9	1505	17	US-10-172-118-1120
6	1359.4	99.9	1505	17	US-10-342-887-1120
7	1359.4	99.9	1505	18	US-10-755-889-277
8	1359.4	99.9	1520	9	US-09-729-402-7
9	1359.4	99.9	1520	14	US-10-003-978A-7
10	1358.6	99.8	1964	18	US-10-741-601-90
11	1355.6	99.6	1845	18	US-10-741-601-89

12	1323	97.2	1323	18	US-10-415-682B-1	Sequence 1, Appli
13	1162.4	85.4	1335	9	US-09-729-402-30	Sequence 30, Appl
14	1162.4	85.4	1335	14	US-10-003-978A-30	Sequence 30, Appl
15	1049.6	77.1	1533	9	US-09-729-402-23	Sequence 23, Appl
16	1049.6	77.1	1533	14	US-10-003-978A-23	Sequence 23, Appl
17	1043.2	76.6	2191	9	US-09-729-402-22	Sequence 22, Appl
18	1043.2	76.6	2191	14	US-10-003-978A-22	Sequence 22, Appl
19	783.6	57.6	1494	9	US-09-729-402-21	Sequence 21, Appl
20	783.6	57.6	1494	14	US-10-003-978A-21	Sequence 21, Appl
21	538.4	39.6	580	9	US-09-729-402-26	Sequence 26, Appl
22	538.4	39.6	580	14	US-10-003-978A-26	Sequence 26, Appl
23	524.2	38.5	572	9	US-09-922-067-8	Sequence 8, Appli
24	524.2	38.5	572	15	US-10-173-233-8	Sequence 8, Appli
25	524.2	38.5	572	16	US-10-406-156-8	Sequence 8, Appli
26	426.6	31.3	477	10	US-09-918-995-24863	Sequence 24863, A
27	410	30.1	1876	9	US-09-729-402-24	Sequence 24, Appl
28	410	30.1	1876	14	US-10-003-978A-24	Sequence 24, Appl
C	390.2	28.7	420	9	US-09-922-067-5	Sequence 5, Appli
C	390.2	28.7	420	15	US-10-173-233-5	Sequence 5, Appli
C	390.2	28.7	420	16	US-10-406-156-5	Sequence 5, Appli
32	307.6	22.6	517	9	US-09-729-402-25	Sequence 25, Appl
33	307.6	22.6	517	14	US-10-003-978A-25	Sequence 25, Appl
34	302.8	22.2	379	9	US-09-922-067-6	Sequence 6, Appli
35	302.8	22.2	379	15	US-10-173-233-6	Sequence 6, Appli
36	302.8	22.2	379	16	US-10-406-156-6	Sequence 6, Appli
37	275.4	20.2	279	9	US-09-922-067-7	Sequence 7, Appli
38	275.4	20.2	279	15	US-10-173-233-7	Sequence 7, Appli
39	275.4	20.2	279	16	US-10-406-156-7	Sequence 7, Appli
C	238.6	17.5	385	9	US-09-962-832-58	Sequence 58, Appl
C	238.6	17.5	385	11	US-09-880-107-1974	Sequence 1974, Ap
C	238.6	17.5	385	11	US-09-968-007A-185	Sequence 185, App
43	234.6	17.2	437	9	US-09-960-352-10049	Sequence 10049, A
C	234.4	17.2	441	10	US-09-918-995-13782	Sequence 13782, A
45	211.2	15.5	317	9	US-09-960-352-13450	Sequence 13450, A

ALIGNMENTS

RESULT 1
US-09-922-067-9
; Sequence 9, Application US/09922067
; Patent No. US2002017209A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
; TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
; Thereof And Use Of The Same In Diagnosis And Therapy
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,067
; FILING DATE: 03-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/193,130
; FILING DATE: 1998-11-17

QY 601 CTATTTCAAGGACCAATCTGTCAGAAATAGGGGACAAAGTCTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGTCAGAAATAGGGGACAAAGTCTGGCTCTACCTTAGAAC 784
QY 661 CCTGAAACAAGGAGGAGACACATATACGAATAGCAGGTACGGCAAGCAAGCAAGAA 720
Db 785 CCTGAAACAAGGAGGAGACACATATACGAATAGCAGGTACGGCAAGCAAGCAAGAA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTTTCAGATTTGATGATGATGATGATGATGAT 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTTTCAGATTTGATGATGATGATGATGATGAT 904
QY 781 ATTAGATTTAAAGTTTGTATGGAACAACCTGAAGGACTCTATTGATAGGAAAAAATAGC 840
Db 905 ATTAGATTTAAAGTTTGTATGGAACAACCTGAAGGACTCTATTGATAGGAAAAAATAGC 964
QY 841 AGTAATTGGACATTTTGTGGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 965 AGTAATTGGACATTTTGTGGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
QY 901 ATTGAGATGTTGATTTGCCCTGGATGATGATGATGATGATGATGATGATGATGAT 960
Db 1025 ATTGAGATGTTGATTTGCCCTGGATGATGATGATGATGATGATGATGATGATGAT 1084
QY 961 CAGAAATCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTAATAT 1020
Db 1085 CAGAAATCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTAATAT 1144
QY 1021 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGG 1080
Db 1145 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGG 1204
QY 1081 TTCAGTCCACCAAGATTTTGTGACTTCACTTTTGCAACTGGCAAAATATTGGACACAT 1140
Db 1205 TTCAGTCCACCAAGATTTTGTGACTTCACTTTTGCAACTGGCAAAATATTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGAGCTATTGATCTTAGCAAAAGCTTC 1200
Db 1265 GCTCAAAATTAAGGGAGACATAGATTCAAAATGAGCTATTGATCTTAGCAAAAGCTTC 1324
QY 1201 ATTAGCATTTTACAAAAGCATTTAGGACTTCATAAAGATTTTATGATGATGATGAT 1260
Db 1325 ATTAGCATTTTACAAAAGCATTTAGGACTTCATAAAGATTTTATGATGATGATGAT 1384
QY 1261 GATTGAAGGAGATGATGAGATCTTATTCAGGGACCAACATTAAACAAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGATCTTATTCAGGGACCAACATTAAACAAACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 9
US-10-003-978A-7

; Sequence 7, Application US/10003978A
; Publication No. US20030072747A1

; GENERAL INFORMATION:

; APPLICANT: Cousins, Lawrence S.

; Eberhardt, Christine D.

; Gray, Patrick W.

; Le Trong, Hai

; Tjoelker, Larry W.

; Wilder, Cheryl L.

; TITLE OF INVENTION: Platelet-Activating Factor

; Acetylhydrolase

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, Gerstein & Borun

; STREET: 5300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America
; ZIP: 60606-6357
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/003,978A
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/729,402
; FILING DATE: 04-DEC-2000
; APPLICATION NUMBER: US 09/577,758
; FILING DATE: 23-MAY-2000
; APPLICATION NUMBER: US 09/010,715
; FILING DATE: 22-JAN-1998
; APPLICATION NUMBER: US 08/480,658
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030072747A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/37792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-003-978A-7

Query Match 99.9%; Score 1359.4; DB 14; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCCAAAATTCATGT 60
Db 125 TGAGAGACTAAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCCAAAATTCATGT 184
QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 185 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGC 180
Db 245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTAAATATCCCGGGGAAATGGGCTTATTCCTGTTGGTTGTAC 240
Db 305 TGCAAGCTTTGGCCAAACTAAATATCCCGGGGAAATGGGCTTATTCCTGTTGGTTGTAC 364
QY 241 AGACTTAATGTTTGTATCAGCACTAATAAGGGCACCTTCCTGCTTTATATATCCATCCCA 300
Db 365 AGACTTAATGTTTGTATCAGCACTAATAAGGGCACCTTCCTGCTTTATATATCCATCCCA 424
QY 301 AGATAATGATCGCTTGACACCTTTTGGATCCCAAAATAAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCTTGACACCTTTTGGATCCCAAAATAAAGAAATATTTTGGGGTCTTAG 484
QY 361 CAAATTTCTTGAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420

Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGTTACTCTTTGGTTCAAT 544
QY 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAATAATATCCACTTGTGT 480
Db 545 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAATAATATCCACTTGTGT 604
QY 481 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTAATCTGCTATTGGCATTTGACCTGGC 540
Db 605 TTTTCTCATGGTCTTGGGGCATTCAGGACACTTTAATCTGCTATTGGCATTTGACCTGGC 664
QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACAACAGAGATAGATCTGCATCTGCAACTTA 600
Db 665 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACAACAGAGATAGATCTGCATCTGCAACTTA 724
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAGTCTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAGTCTTGGCTCTACCTTAGAAC 784
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 785 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 904
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840
Db 905 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 964
QY 841 AGTAATTGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 965 AGTAATTGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
QY 901 ATTCAGATGTTGATTTGCCCTGGATGATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTTGATTTGCCCTGGATGATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATTCCTCAGCCCCCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCCCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1144
QY 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080
Db 1145 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1204
QY 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACCTTTGCAACTGGCAAAATATTTGGACACAT 1140
Db 1205 TTCAGTCCACCAGAAATTTTGTGACTTCACCTTTGCAACTGGCAAAATATTTGGACACAT 1264
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAAAAGCTTC 1200
Db 1265 GCTCAAAATTAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTAGCAAAAGCTTC 1324
QY 1201 ATTAGCATTTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATTTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGATCTTATCCAGGGACCAACATTAAACAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGATCTTATCCAGGGACCAACATTAAACAACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 10

US-10-741-601-90
; Sequence 90, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-90

Query Match 99.8%; Score 1358.6; DB 18; Length 1964;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1355; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTTGCATGT 60
Db 261 TGAGAGACTAAGCTGAAACTGCTGCTYAGCTCCCAAGATGGTGCCACCCAAATTTGCATGT 320
QY 61 GCTTTTCTGCCTCTGCGGCTGCCTGGCTGTGTTTATCTTTTGTGCTGCAATACATAAA 120
Db 321 GCTTTTCTGCCTSTGCGGCTGCCTGGCTGTGTTTATCTTTTGTGCTGCAATACATAAA 380
QY 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGC 180
Db 381 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGC 440
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGAAATGGGCCCTTATTCGGTTGGTTGTAC 240
Db 441 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGAAATGGGCCCTTATTCGGTTGGTTGTAC 500
QY 241 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTTCTGCGTTTATATTTATCCATCCCA 300
Db 501 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTTCTGCGTTTATATTTATCCATCCCA 560
QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 561 AGATAATGATCCTTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 620
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 621 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 680
QY 421 GACAACTCCTGCAAACTGGAAATTCCTCTGAGGCCCTGGTGAATAATATCCACTTGTGT 480
Db 681 GACAACTCCTGCAAACTGGAAATTCCTCTGAGGCCCTGGTGAATAATATCCACTTGTGT 740
QY 481 TTTTCTCATGGTCTTTGGGGCATTCAGGACACTTTTATCTGCTATTGGCATTTGACCTGGC 540
Db 741 TTTTCTCATGGTCTTTGGGGCATTCAGGACACTTTTATCTGCTATTGGCATTTGACCTGGC 800
QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db 801 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 860
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAGTCTTGGCTCTACCTTAGAAC 660
Db 861 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAGTCTTGGCTCTACCTTAGAAC 920
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
Db 921 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 980
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
Db 981 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGATGC 1040
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 840
Db 1041 ATTAGATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAATAATAGC 1100

```
QY 841 AGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
Db 1101 AGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1160

QY 901 ATTGAGATGTGGTATGCCCCCTGGATGATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1161 ATTGAGATGTGGTATGCCCCCTGGATGATGGATGTTTCCACTGGGTGATGAAGTATATTC 1220

QY 961 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1020
Db 1221 CAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATAT 1280

QY 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAAATCAGGGG 1080
Db 1281 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAAATCAGGGG 1340

QY 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCACCTGATTTGCAACTGGCAAAATAATTGGACACAT 1140
Db 1341 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCACCTGATTTGCAACTGGCAAAATAATTGGACACAT 1400

QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1401 GCTCAAAATTAAGGGAGACATAGATTCAAAATGVAGCTATTGATCTTAGCAACAAAGCTTC 1460

QY 1201 ATTAGCATCTTACAAAAGCAATTTAGGACTTCTATAAGATTTTGTGATCAGTGGGACTGCTT 1260
Db 1461 ATYAGCATCTTACAAAAGCAATTTAGGACTTCTATAAGATTTTGTGATCAGTGGGACTGCTT 1520

QY 1261 GATTGAAGGAGATGATGAGAACTTTATTTCCAGGACCAACATTAACAAACCAATCAACA 1320
Db 1521 GATTGAAGGAGATGATGAGAACTTTATTTCCAGGACCAACATTAACAAACCAATCAACA 1580

QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1581 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1621
```

RESULT 11

US-10-741-601-89

```
; Sequence 89, Application US/10741601
; Publication No.: US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 1845
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-89
```

```
Query Match 99.6%; Score 1355.6; DB 18; Length 1845;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1352; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTGCATGTGCT 63
Db 145 GAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCCAAAATTGCATGTGCT 204

QY 64 TTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 123
Db 205 TTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 264

QY 124 TGTGCCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGCTGC 183
Db 265 TGTGCCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGCTGC 324
```

```
QY 184 AAGCTTTGGCCAAAATAAAATCCCGGGGAAATGGGCCCTTATTCGGTTGGTTGTACAGA 243
Db 325 AAGCTTTGGCCAAAATAAAATCCCGGGGAAATGGGCCCTTATTCGGTTGGTTGTACAGA 384

QY 244 CTTAATGTTTGTATCACACTAAATAAGGGCACCTTCTTGGTTCGTTTATATATCCATCCCAAGA 303
Db 385 CTTAATGTTTGTATCACACTAAATAAGGGCACCTTCTTGGTTCGTTTATATATCCATCCCAAGA 444

QY 304 TAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATAATTTTGGGGCTTTAGCAA 363
Db 445 TAATGATRCCTTGACACCCCTTTGGATCCCAATAAAGAATAATTTTGGGGCTTTAGCAA 504

QY 364 ATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGGTTACTCTTTGGTTCAATGAC 423
Db 505 ATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGGTTACTCTTTGGTTCAATGAC 564

QY 424 AACTCCTGCAAACTGGAATTCCTCTGAGGCTGGTGAAAAATATCCACTTGTGTGTTTT 483
Db 565 AACTCCTGCAAACTGGAATTCCTCTGAGGCTGGTGAAAAATATCCACTTGTGTGTTTT 624

QY 484 TTCTCATGGTCTTGGGGCAATTCAGGACACTTTATTTCTGCTATTGGCATTTGACCTGGCATC 543
Db 625 TTCTCATGGTCTTGGGGCAATTCAGGACACTTTATTTCTGCTATTGGCATTTGACCTGGCATC 684

QY 544 TCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTACTA 603
Db 685 TCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTACTA 744

QY 604 TTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTTAGAACCTT 663
Db 745 TTTCAAGGACCAATCTGCTGCAGAAAYAGGGGCAAGTCTTGGCTCTACCTTTAGAACCTT 804

QY 664 GAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAAAGAGCAAAAGAATG 723
Db 805 GAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAAAGAGCAAAAGAATG 864

QY 724 TTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGAATGCATT 783
Db 865 TTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGAATGCATT 924

QY 784 AGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGGAAGAAATPAGCAGT 843
Db 925 AGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGGAAGAAATPAGCAGT 984

QY 844 AATTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATT 903
Db 985 AATTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATT 1044

QY 904 CAGATGTGTTATGCCCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAG 963
Db 1045 CAGATGTGTTATGCCCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAG 1104

QY 964 AATTCTCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTGCTAATATCAT 1023
Db 1105 AATTCTCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTGCTAATATCAT 1164

QY 1024 AAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTT 1083
Db 1165 AAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTT 1224

QY 1084 AGTCCACCAGAAATTTTGTGCTGCTTCACTTTTGGCAACTGGCAAAATAATTGGACATGCT 1143
Db 1225 AGTCCACCAGAAATTTTGTGCTGCTTCACTTTTGGCAACTGGCAAAATAATTGGACATGCT 1284

QY 1144 CAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATT 1203
Db 1285 CAAATTAAGGGAGACATAGATTCAAATGYAGCTATTGATCTTAGCAACAAAGCTTCATY 1344

QY 1204 AGCATTTCTTACAAAAGCATTTTAGGACTTTCATAAAGATTTTGTAGTGGGACTGCTTGAT 1263
Db 1345 AGCATTTCTTACAAAAGCATTTTAGGACTTTCATAAAGATTTTGTAGTGGGACTGCTTGAT 1404

QY 1264 TGAAGGAGATGATGAGAAATCTTATTCAGGGGACCAACATTAACACAAACCAATCAACAT 1323
```

Db 1405 TGAAGGAGATGATGAGAACTTTATCCAGGGACCAACATTAAACAAACCAATCAACACAT 1464
QY 1324 CATGTTACAGAACTCTTTCAGGAATAGAGAATAACAATT 1361
Db 1465 CATGTTACAGAACTCTTTCAGGAATAGAGAATAACAATT 1502

RESULT 12

US-10-415-682B-1
; Sequence 1, Application US/10415682B
; Publication No. US20040259087A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, David
; APPLICANT: McGinnis, Ralph
; APPLICANT: Spurr, Nigel
; APPLICANT: Valdes, Ana, Maria
; TITLE OF INVENTION: METHOD AND KIT TO DETERMINE LP-PLA2
; TITLE OF INVENTION: POLYMORPHIC VARIANTS ASSOCIATED WITH SUSCEPTIBILITY TO
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: P32704
; CURRENT APPLICATION NUMBER: US/10/415,682B
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: PCT/GB01/04876
; PRIOR FILING DATE: 2001-02-11
; PRIOR APPLICATION NUMBER: GB 0027181.7
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-415-682B-1

Query Match 97.2%; Score 1323; DB 18; Length 1323;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 ATGGTGCCACCCAAATTCGATGTGCTTTCTGCCTCTCGGCTGCCTGGCTGTGTTTAT 97
Db 1 ATGGTGCCACCCAAATTCGATGTGCTTTCTGCCTCTCGGCTGCCTGGCTGTGTTTAT 60
QY 98 CCTTTTGACTGGCAATACATAAATCCTGTGGCCCATATGAATCATCAGATGGTCAAC 157
Db 61 CCTTTTGACTGGCAATACATAAATCCTGTGGCCCATATGAATCATCAGATGGTCAAC 120
QY 158 AAATACAACTAGTGTGCTGCAAGCTTTGGCCAACTAAATCCCGGGGAAAT 217
Db 121 AAATACAACTAGTGTGCTGCAAGCTTTGGCCAACTAAATCCCGGGGAAAT 180
QY 218 GGGCCTTATCCGTTGGTTGACAGACTTAATGTTTGATCACACTAATAAGGGCACCTTC 277
Db 181 GGGCCTTATCCGTTGGTTGACAGACTTAATGTTTGATCACACTAATAAGGGCACCTTC 240
QY 278 TTGCGTTTATATTATCCATCCCAAGATAATGATCGCCTTGACACCCCTTTGGATCCCAAT 337
Db 241 TTGCGTTTATATTATCCATCCCAAGATAATGATCGCCTTGACACCCCTTTGGATCCCAAT 300
QY 338 AAAGAATATTTTGGGCTTTAGCAAAATTTCTTGAACACACTGGCTTATGGGCAACAT 397
Db 301 AAAGAATATTTTGGGCTTTAGCAAAATTTCTTGAACACACTGGCTTATGGGCAACAT 360
QY 398 TTGAGGTTACTCTTTGGTTCAATGACAACTCCTGCAAACTGGAATTCCTCTGAGGCCT 457
Db 361 TTGAGGTTACTCTTTGGTTCAATGACAACTCCTGCAAACTGGAATTCCTCTGAGGCCT 420
QY 458 GGTGAAAAATATCCACTTGTGTTTCTCATGGTCTTGGGGCAATTCAGGACACTTTAT 517
Db 421 GGTGAAAAATATCCACTTGTGTTTCTCATGGTCTTGGGGCAATTCAGGACACTTTAT 480
QY 518 TCTGCTATTGGCATTGACCTGGCATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGA 577

Db 481 TCTGCTATTGGCATTGACCTGGCATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGA 540
QY 578 GATAGATCTGCATCTGCAACTTACTATTCAAGGACCACCAATCTGCTGCAGAAATAGGGGAC 637
Db 541 GATAGATCTGCATCTGCAACTTACTATTCAAGGACCACCAATCTGCTGCAGAAATAGGGGAC 600
QY 638 AAGTCTTGGCTCTACCTTTAGAACCCCTGAAACAGAGAGGAGACACATATACGAATGAG 697
Db 601 AAGTCTTGGCTCTACCTTTAGAACCCCTGAAACAGAGAGGAGACACATATACGAATGAG 660
QY 698 CAGGTACGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGAT 757
Db 661 CAGGTACGCAAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGAT 720
QY 758 CATGGAAGCCAGTGAAGATGCATTAGATTAAAGTTTGATATGGAACCACTGAAGGAC 817
Db 721 CATGGAAGCCAGTGAAGATGCATTAGATTAAAGTTTGATATGGAACCACTGAAGGAC 780
QY 818 TCTATTGATAGGGAAAAATAGCAGTAATTGGACATTCTTTTGGTGAGCAACGGTTATT 877
Db 781 TCTATTGATAGGGAAAAATAGCAGTAATTGGACATTCTTTTGGTGAGCAACGGTTATT 840
QY 878 CAGACTCTTAGTGAAGATCAGAGATTTCAGATGTGGTATTCCTTGGATGGATGGATGTTT 937
Db 841 CAGACTCTTAGTGAAGATCAGAGATTTCAGATGTGGTATTCCTTGGATGGATGGATGTTT 900
QY 938 CCACCTGGGTGATGAAGTATATTCCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAA 997
Db 901 CCACCTGGGTGATGAAGTATATTCCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAA 960
QY 998 TATTTCCAAATATCCTGCTAATATCATAAAAATGAAAAATGCTACTCCTCTGATAAGAA 1057
Db 961 TATTTCCAAATATCCTGCTAATATCATAAAAATGAAAAATGCTACTCCTCTGATAAGAA 1020
QY 1058 AGAAAGATGATTACAATCAGGGGTTCACTCCACCAGAAATTTGCTGACTTCACTTTTGCA 1117
Db 1021 AGAAAGATGATTACAATCAGGGGTTCACTCCACCAGAAATTTGCTGACTTCACTTTTGCA 1080
QY 1118 ACTGGCAAAATAATTGGACACATGCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCT 1177
Db 1081 ACTGGCAAAATAATTGGACACATGCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCT 1140
QY 1178 ATTGATCTTAGCAACAAAGCTTCATTAGCATTCTTACAAAAGCATTTAGGACTTCATAAA 1237
Db 1141 ATTGATCTTAGCAACAAAGCTTCATTAGCATTCTTACAAAAGCATTTAGGACTTCATAAA 1200
QY 1238 GATTTTGATCAGTGGGACTGCTTGATTGAAGGAGATGATGAGAACTTTATCCAGGGACC 1297
Db 1201 GATTTTGATCAGTGGGACTGCTTGATTGAAGGAGATGATGAGAACTTTATCCAGGGACC 1260
QY 1298 AACATTAAACAAACCAATCAACACATCATGTTACAGAACTCTTCAGGAATAGAGAAATAC 1357
Db 1261 AACATTAAACAAACCAATCAACACATCATGTTACAGAACTCTTCAGGAATAGAGAAATAC 1320
QY 1358 AAT 1360
Db 1321 AAT 1323

RESULT 13

US-09-729-402-30
; Sequence 30, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,402
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20010021379Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-729-402-30

Query Match 85.4%; Score 1162.4; DB 9; Length 1335;
Best Local Similarity 92.4%; Pred. No. 1.5e-309;
Matches 1223; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 38 ATGGTGCCACCAAAATTGCATGTGCTTTCTGCTCTGCGGCTGCGCTGCTGCTGCTTTAT 97
Db 1 ATGGTACCCCAAGCTGCACGCTGCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAC 60
QY 98 CCTTTTGACTGGCAATACATAAATCTGTTGCCATATGAATCATCATCAGATGGGTCAAC 157
Db 61 CCTTCGATTGGCAGTATATCAACCCCGTGGCTCACATGAAGCAGCGCTGGGTGAAT 120
QY 158 AAAATACAAGTACTGATGGCTGGTCAAGCTTTGGCCAAACTAAATCCCGGGGAAAT 217
Db 121 AAGATCCAGGTGCTCATGGCCGACCAAGCTTCGGTCAGACCAAGATTCTCTAGAGGCAAC 180
QY 218 GGGCCTTATTCGGTGGTGTGACAGACTTAATGTTGATCAGACTAATAAGGCACTTC 277
Db 181 GGCCCTTACAGCGTGGGCTGCACGATCTGTATGTTTCGACCATACCAACAAAGGAACCTTT 240
QY 278 TTGCGTTTATATTTATCCATCCCAAGATAAATGATGCGCTTGACACCTTTTGGATCCCAAT 337
Db 241 CTGAGACTGTACTACCCCGAGCCAGGACCAACGACAGACTGGATACTCTGTGGATCCCAAT 300
QY 338 AAAGAATATTTTGGGCTCTTAGCAAAATTTCTTGAACACACACTGGCTTATGGGCAACATT 397
Db 301 AAAGAATATTTTGGGCTCTTAGCAAAATTTCTTGAACACACACTGGCTTATGGGCAACATT 360
QY 398 TTGAGGTTACTCTTTGGTTCAATGACAACTCCCTGCAAACTGGAAATCCCTCTGAGGCCT 457
Db 361 TTGAGGTTACTCTTTGGTTCAATGACAACTCCCTGCAAACTGGAAATCCCTCTGAGGCCT 420
QY 458 GGTGAAAAATATCCACTTGTGTTTCTCATGCTTTGGGGCATTCAGGACACTTTAT 517

Db 421 GGTGAAAAATATCCACTTGTGTGTTTTTTCTCATGGTCTTGGGGCATTCAGGACACTTTAT 480
QY 518 TCTGCTATTGGCATTGACCTGGCATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGA 577
Db 481 TCTGCTATTGGCATTGACCTGGCATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGA 540
QY 578 GATAGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 637
Db 541 GATAGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 600
QY 638 AAGTCTTGGCTCTACCTTAGAACCCCTGAAACAGAGGAGGAGACACATATACGAAATGAG 697
Db 601 AAGTCTTGGCTCTACCTTAGAACCCCTGAAACAGAGGAGGAGACACATATACGAAATGAG 660
QY 698 CAGGTACGGCAAAAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGATTCTTGCATTGAT 757
Db 661 CAGGTACGGCAAAAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGATTCTTGCATTGAT 720
QY 758 CATGGAAGCCAGTGAAGATGCATTAGATTAAAGTTTGAATATGGAACAACTGAAGGAC 817
Db 721 CATGGAAGCCAGTGAAGATGCATTAGATTAAAGTTTGAATATGGAACAACTGAAGGAC 780
QY 818 TCTATTGATAGGGAAAAAATAGCAGTAATTTGGAACATTTTGGTGGAGCAACGGTTATT 877
Db 781 TCTATTGATAGGGAAAAAATAGCAGTAATTTGGAACATTTTGGTGGAGCAACGGTTATT 840
QY 878 CAGACTCTTAGTGAAGATCAGAGATTTCAGATGTGGTATTGCCCTGGATGCGATGTTT 937
Db 841 CAGACTCTTAGTGAAGATCAGAGATTTCAGATGTGGTATTGCCCTGGATGCGATGTTT 900
QY 938 CCACTGGGTGATGAAGTATATTCCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAA 997
Db 901 CCACTGGGTGATGAAGTATATTCCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAA 960
QY 998 TATTTCCAATATCTGCTAATATCATAAATAATGAAAAAATGCTACTCACCTGATAAAGAA 1057
Db 961 TATTTCCAATATCTGCTAATATCATAAATAATGAAAAAATGCTACTCACCTGATAAAGAA 1020
QY 1058 AGAAAGATGATTACAATCAGGGGTTTCAGTCCACAGAAATTTTGTGCTGACTTCACTTTTGA 1117
Db 1021 AGAAAGATGATTACAATCAGGGGTTTCAGTCCACAGAAATTTTGTGCTGACTTCACTTTTGA 1080
QY 1118 ACTGGCAAAATAATTTGGACACATGCTCAAAATTTAAAGGGAGACATAGATTCAAATGCTAGCT 1177
Db 1081 ACTGGCAAAATAATTTGGACACATGCTCAAAATTTAAAGGGAGACATAGATTCAAATGCTAGCT 1140
QY 1178 ATTGATCTTAGCAACAAAGCTTCATTAGCAATTTTCAAAAGCATTTTAGGACTTCATAAA 1237
Db 1141 ATTGATCTTAGCAACAAAGCTTCATTAGCAATTTTCAAAAGCATTTTAGGACTTCATAAA 1200
QY 1238 GATTTTGTGATCAGTGGGACTGCTGATTGAAGGAGATGATGAGAATCTTATCCAGGGGACC 1297
Db 1201 GATTTTGTGATCAGTGGGACTGCTGATTGAAGGAGATGATGAGAATCTTATCCAGGGGACC 1260
QY 1298 AACATTAAACACAAACCAATCAACACATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATAC 1357
Db 1261 AACATTAAACACAAACCAATCAACACATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATAC 1320
QY 1358 AATT 1361
Db 1321 AATT 1324

RESULT 14
US-10-003-978A-30
; Sequence 30, Application US/10003978A
; Publication No. US20030072747A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.

RESULT 15
US-09-729-402-23
; Sequence 23, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,402
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20010021379Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1533 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 62..1394
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-729-402-23

Query Match 77.1%; Score 1049.6; DB 9; Length 1533;
Best Local Similarity 86.2%; Pred. No. 2.1e-278;
Matches 1173; Conservative 0; Mismatches 184; Indels 3; Gaps 1;
QY 5 AGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATGCGATGCTT 64
DB 29 AGGTTAAGCTGAAACGGCAGCTCAGCTTCGGAGATGTTACCGTCCAAATGCGATGCTT 88
QY 65 TTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 124
DB 89 TTCTGCTCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 148
QY 125 GTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAAGTACTGATGGCTGCTGCA 184
DB 149 GTTGCCATATTGAATCACCAGCATGGGTTCAGTAAGATACAAAGCTCTGATGGCTGCTGCA 208

QY 185 AGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCCCTTATTCCGTTGGTTGTACAGAC 244
DB 209 AACATTGGTCAATCTAAATCCCGAGAGGAATGGATCTTATCCGTCGGTTGTACAGAC 268
QY 245 TTAATGTTTGATCACACTAATAAGGGCACCTCTTTCGCTTATATTATCCATCCCAAGAT 304
DB 269 TTGATGTTTGATTACACTAATAAGGGCACCTCTTTCGCTTATATTATCCATCTCAAGAT 328
QY 305 AATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAGCAAA 364
DB 329 GATGATCACTCCGACACCCCTTTGGATCCCAACAAAGAAATATTTTGGGTCTTAGTAAA 388
QY 365 TTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTTGGTTCAATGACA 424
DB 389 TTTCTTGGAAACACACTGGCTTATGGGCAAAATATATGGGCTTATCTTCGGTTCAATGACA 448
QY 425 ACTCTGCAAACTGGAATTCCTCTCTGAGGCTGGTGAATAATATCCACTTGTGTTTTT 484
DB 449 ACTCTGCAAGCTGGAATGACATCTGAGGACTGGGAAATAATACCCACTAATATTTTT 508
QY 485 TCTCATGGTCTTGGGGCATTCAGGACACATTTATTTCTGCTATTTGGCATTTGACCTGGCATCT 544
DB 509 TCTCATGGTCTTGGAGCAATCAGGACGATTTATTTCTGCTATTTGGCATTTGATCTGGCATCC 568
QY 545 CATGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCTATCTGCACTTACTAT 604
DB 569 CACGGTTTATAGTTGCTGTGTAGAACACAGGATGGCTCTGCTATCTCGACATACTAT 628
QY 605 TTCAAGGACCAATCTGCTGAGAAATAGGGACAAAGTCTTGGCTCTACCTTGAACCCCTG 664
DB 629 TTCAAGGACCAAGTCTGCTGTAGAAATAGGCAACAAAGTCTTGGCTCTATCTCAGAACCCCTG 688
QY 665 AA--ACAAGAGGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGAA 721
DB 689 AAGCGAGGAGAGGAGGAGTTTCTTTTACGAATGAGCAGTTACGGCAACGAGCAAAAGGAA 748
QY 722 TGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAGCCAGTGAAGAATGCA 781
DB 749 TGTTCTCAAGCTCTCAGTTTGTGATTTCTGGACATTTGATCACGGAGGCCAGTGAAGAATGTA 808
QY 782 TTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGGAATAAATAGCA 841
DB 809 CTAGATTTAGAGTTTGATGTGGAACAGCTGAAGGACTCTATTGATAGGGATAAATAGCC 868
QY 842 GTAATTGGACATTTTGTGGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGA 901
DB 869 ATTATTGGACATTTTGTGGGAGCCACAGTTATTTCAGACTCTTAGTGAAGACAGAGA 928
QY 902 TTCAGATGTGTTATGCTGCTGATGATGATGATGATTTCCACTGGGTGATGAAGTATATTC 961
DB 929 TTCAGGTGTGCTATGCTCTGATGATGATGATGATTTCCCGTGGGTGATGAAGTATATTC 988
QY 962 AGAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATC 1021
DB 989 AGAATTCCTCAACCCCTCTTTTATCAACTCGGAACGATTTCCAATACCCCTTCTAATATC 1048
QY 1022 ATAAAAATGAAAAAATGCTACTCCTGATGATGATGATGATGATGATGATGATGATGATGAT 1081
DB 1049 ATAAGAATGAAAAAATGCTTCTTACCTGATAGAGAACGAAAAATGATTAACAATCAGGGGT 1108
QY 1082 TCAGTCCACCAAGAAATTTTGTGCTGCTTCACTTTTGCCTGCAACTGGCAAAATAATGGAACATG 1141
DB 1109 TCGGTCCATCAGAAATTTTGTGCTGCTTCACTTTTGCCTGCAACTAGCAAAATAATGGAACATG 1168
QY 1142 CTCAAAATTAAGGAGACATAGATTTCAATGCACTATTGATCTTTAGCAACAAGCTTCA 1201
DB 1169 TTCACACTGAAGGAGACATGATTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1228
QY 1202 TTAGCATTTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGTGATCAGTGGGACTGCTTG 1261
DB 1229 TTAGCGTTTTCACAAAACATTTAGGACTTTCAGAAAGATTTTGTGATCAGTGGGACTTTTA 1288
QY 1262 ATTGAAGGAGATGATGAGAAATCTTATTCAGGAGCAACATTTAACAACAACCAATCAACAC 1321

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:21 ; Search time 5497.71 Seconds
(without alignments)
9423.093 Million cell updates/sec

Title: US-09-922-067F-9
Perfect score: 1361
Sequence: 1 tgagagactaagctgaaact.....aggaatagagaatacaatt 1361

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1351.4	99.3	1562	3	CR608325 full-length
2	1348.4	99.1	1793	3	BC025674 Homo sapi
3	1346.4	98.9	1531	3	CR615354 full-length
4	1255	92.2	1326	9	AY407445 Homo sapi
5	1247	91.6	1326	9	AY407446 Homo sapi
6	920.2	67.6	1022	1	AL575852 AL575852
7	888.4	65.3	1158	3	CR608291 full-length
8	881	64.7	946	1	AL573565 AL573565
9	856.6	62.9	1011	1	AL554852 AL554852
10	808.2	59.4	1890	3	AK051454 Mus muscu
11	785.2	57.7	1695	3	AK005210 Mus muscu
12	761.2	55.9	1007	1	AL552617 AL552617
13	747.6	54.9	935	1	AL549288 AL549288
14	738.2	54.2	1326	9	AY407447 Mus muscu
15	692.4	50.9	734	6	CA312081 UI-CF-FNO
16	643.6	47.3	1376	3	AK005158 Mus muscu
17	609	44.7	796	5	BX926110 BX926110
18	592.4	43.5	594	7	CK903738 ie64e09.y
19	590.2	43.4	900	4	BG530083 602558743
20	583.2	42.9	825	4	BI768378 603053686
21	571.2	42.0	650	1	AI343491 tb97c04.x
22	566.6	41.6	835	5	BP168449 BP168449
23	565.4	41.5	818	5	BX330257 BX330257
24	552.4	40.6	554	4	BI964070 ie64e09.y

25	550	40.4	584	5	BP296533	BP296533
26	538	39.5	560	4	BM788963	BM788963 K-EST0068
27	529.6	38.9	874	4	BI182205	BI182205 UNL-P-FN-
28	529.2	38.9	733	4	BI912346	BI912346 603067687
29	513.6	37.7	598	2	BF509203	BF509203 UI-H-BI4-
30	497.4	36.5	519	2	AW071677	AW071677 ws53b01.x
31	490.4	36.0	875	4	BI688832	BI688832 603311546
32	486.2	35.7	751	5	BP439513	BP439513 BP439513
33	483.8	35.5	560	2	BF508812	BF508812 UI-H-BI4-
34	481.2	35.4	622	4	BM536645	BM536645 ha72f11.g
35	475.6	34.9	849	7	CK022811	CK022811 AGENCOURT
36	475	34.9	934	5	BU506078	BU506078 AGENCOURT
37	474.2	34.8	858	4	BI772693	BI772693 603053447
38	472.4	34.7	561	5	BP301477	BP301477 BP301477
39	467	34.3	505	5	BQ011547	BQ011547 UI-1-BC1p
40	463.2	34.0	679	5	BP459594	BP459594 BP459594
41	462.6	34.0	708	5	BP147696	BP147696 BP147696
42	461.4	33.9	876	4	BI665978	BI665978 603287028
43	454.8	33.4	750	4	BI689361	BI689361 603315803
44	451.6	33.2	619	7	CK953402	CK953402 4093395 B
45	449.2	33.0	995	6	BY705386	BY705386 BY705386

ALIGNMENTS

RESULT 1
CR608325
LOCUS CR608325 1562 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODI067YM18 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR608325
VERSION CR608325.1 GI:50489132
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1562)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1562)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES Location/Qualifiers
source 1. .1562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI067YM18"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 99.3%; Score 1351.4; DB 3; Length 1562;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1352; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGTCCCAAGATGTCGCCACCCAAATTCATGT 60
|||||
Db 210 TGAGAGACTAAGCTGAACTGCTGCTCAGTCCCAAGATGTCGCCACCCAAATTCATGT 269

QY 61 GCTTTTCTGCTCTGCGGCTGCTGGTGTGTTTATCCCTTTTGACTGGCAATACATAAA 120
Db 270 GCTTTTCTGCTCTGCGGCTGCTGGTGTGTTTATCCCTTTTGACTGGCAATACATAAA 329
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
Db 330 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 389
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGCCCTTATCCGTTGGTTGTAC 240
Db 390 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGCCCTTATCCGTTGGTTGTAC 449
QY 241 AGACTTAATGTTTGATCACACTAATAAGGCACTTCTTGGCTTATATATCCATCCCA 300
Db 450 AGACTTAATGTTTGATCACACTAATAAGGCACTTCTTGGCTTATATATCCATCCCA 509
QY 301 AGATAATGATCGCTTGACACCCCTTGATCCCAATAAAGAAATATTTTGGGCTCTTAG 360
Db 510 AGATAATGATCGCTTGACACCCCTTGATCCCAATAAAGAAATATTTTGGGCTCTTAG 569
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 420
Db 570 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 629
QY 421 GACAACTCCTGCAAACTGGAATCCCTCTGAGGCTGGTGAAATAATCCACTTGTGT 480
Db 630 GACAACTCCTGCAAACTGGAATCCCTCTGAGGCTGGTGAAATAATCCACTTGTGT 689
QY 481 TTTTCTCATGCTTGGGCACTTGGGCACTTATTTCTGCTATGGCAATGACCTGGC 540
Db 690 TTTTCTCATGCTTGGGCACTTGGGCACTTATTTCTGCTATGGCAATGACCTGGC 749
QY 541 ATCTCATGGGTTTATAGTTGCTGTGTAAGAACACAGAGATAGATCTGCACTTGA 600
Db 750 ATCTCATGGGTTTATAGTTGCTGTGTAAGAACACAGAGATAGATCTGCACTTGA 809
QY 601 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660
Db 810 CTATTTCAAGGACCAATCTGCTGCAAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 869
QY 661 CCTGAAACAAGAGGAGAGACACATATACGAATAGCAGGTACGGCAAGAGCAAAAGA 720
Db 870 CCTGAAACAAGAGGAGAGACACATATACGAATAGCAGGTACGGCAAGAGCAAAAGA 929
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTGATGATGATGATGATGATGATGATGATGATG 780
Db 930 ATGTTCCCAAGCTCTCAGTCTGATTTGATGATGATGATGATGATGATGATGATGATG 989
QY 781 ATTAGATTTAAAGTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 990 ATTAGATTTAAAGTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1049
QY 841 AGTAATTGACATTTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG 900
Db 1050 AGTAATTGACATTTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG 1109
QY 901 ATTCAGATGTTGTTATGCTGCTGGATGATGATGATGATGATGATGATGATGATGATG 960
Db 1110 ATTCAGATGTTGTTATGCTGCTGGATGATGATGATGATGATGATGATGATGATGATG 1169
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1020
Db 1170 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATAT 1229
QY 1021 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
Db 1230 CATAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1289
QY 1081 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCAACTGCGCAAAATATTTGGACACAT 1140
Db 1290 TTCAGTCCACCAGAAATTTTGTGACTTCACTTTTGCAACTGCGCAAAATATTTGGACACAT 1349

QY 1141 GCTCAAAATTAAAGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1200
Db 1350 GCTCAAAATTAAAGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTC 1409
QY 1201 ATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
Db 1410 ATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTT 1469
QY 1261 GATTGAAGGAGATGATGAGAACTTTATTCAGGAGGACCAACATTAACACACCAATCAACA 1320
Db 1470 GATTGAAGGAGATGATGAGAACTTTATTCAGGAGGACCAACATTAACACACCAATCAACA 1529
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAA 1353
Db 1530 CATCATGTTACAGAACTCTTCAGGAATAGAGAA 1562

RESULT 2
BC025674
LOCUS
DEFINITION Homo sapiens cDNA clone IMAGE:5203018, containing frame-shift errors.
ACCESSION BC025674
VERSION BC025674.1 GI:19343677
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1793)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lalic, P., Legaspi, R., Maduro, Q. L., Masiello, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P. J., Touchman, J. W., Tsurgeon, C., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E. D.

ORIGIN

Query Match	99.1%;	Score 1348.4;	DB 3;	Length 1793;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1360;	Conservative	0;	Mismatches 1;	Indels 1; Gaps 1;
1	TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCTCCCAAGATGCTGCCACCCAAATTGCATGT	60		
161	TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCTCCCAAGATGCTGCCACCCAAATTGCATGT	220		
61	GCTTTTCTGCCTCTCGGGCTGCCTGGCTGGTTTATCCTTTTGACTGGCAATACATAAA	120		
221	GCTTTTCTGCCTCTCGGGCTGCCTGGCTGGTTTATCCTTTTGACTGGCAATACATAAA	280		
121	TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC	180		
281	TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC	340		
181	TGCAAGCTTTGGCCAAACTTAAATATCCCGGGGAAATGGGCCTTATTCGGTTGGTTGTAC	240		
341	TGCAAGCTTTGGCCAAACTTAAATATCCCGGGGAAATGGGCCTTATTCGGTTGGTTGTAC	400		
241	AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGGGTTTATATTATCCATCCCA	300		
401	AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGGGTTTATATTATCCATCCCA	460		

RESULT 3
CR615354

DEFINITION

ACCESSION

VERSION
KEYWORDS

SOURCE

REFERENCE

AUTHORS	TITLE
---------	-------

JOURNAL
REMARK

REFERENCE

TITLE

11-00000

CR615354 1531 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DI049YE02 of Placenta Cot 25-normalized
of *Homo sapiens* (human).

CR615354.1 GI:50496161

Homo sapiens (human); ENSL1_CDNA:

Homo sapiens

Mammalia; Eut

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Unpublished

contact: Feng Zhang
http://fulllength.in

Faraday Avenue
2 (houses 1 to 1521)

Genoscope.

Submitted (2)

- Web : www.genoscope.cns.fr

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
source Location/Qualifiers
1..1531
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI049YE02"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Query Match 98.9%; Score 1346.4; DB 3; Length 1531;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATTGCATGT 60
DB 184 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATTGCATGT 243

QY 61 GCTTTTCTGCCTCTGCGGCTGCCTGGTGTGGTTTATCCTTTTGACTGGCAATACATAAA 120
DB 244 GCTTTTCTGCCTCTGCGGCTGCCTGGTGTGGTTTATCCTTTTGACTGGCAATACATAAA 303

QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAACTACTGATGCTGC 180
DB 304 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAACTACTGATGCTGC 363

QY 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATCCGTTGGTTGTAC 240
DB 364 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATCCGTTGGTTGTAC 423

QY 241 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTGCGTTTATATATCCATCCCA 300
DB 424 AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTGCGTTTATATATCCATCCCA 483

QY 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTAG 360
DB 484 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTAG 543

QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
DB 544 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 603

QY 421 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAAAAATATCCACTTGTGT 480
DB 604 GACAACTCCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAAAAATATCCACTTGTGT 663

QY 481 TTTTCTCATGGTCTTTGGGCATTTCAGGACACTTTTATCTGCTATTGGCATTTGACCTGGC 540
DB 664 TTTTCTCATGGTCTTTGGGCATTTCAGGACACTTTTATCTGCTATTGGCATTTGACCTGGC 723

QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
DB 724 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 783

QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAACTCTTGGCTCTACCTTAGAAC 660
DB 784 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAACTCTTGGCTCTACCTTAGAAC 843

QY 661 CCTGAAACAAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 720
DB 844 CCTGAAACAAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAGAGCAAAAGA 903

QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTGACATTTGATCATGGAAGCCAGTGAAGAATGC 780
DB 904 ATGTTCCCAAGCTCTCAGTCTGATTTCTGACATTTGATCATGGAAGCCAGTGAAGAATGC 963

QY 781 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTTATTGATAGGAAAAAATAGC 840

DB 964 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGATAGGAAAAAATAGC 1023

QY 841 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
DB 1024 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1083

QY 901 ATTACAGATGTGGTATTGGCCCTGGATGCATGGATGTTTCCACCTGGGTGATGAAGTATATTC 960
DB 1084 ATTACAGATGTGGTATTGGCCCTGGATGCATGGATGTTTCCACCTGGGTGATGAAGTATATTC 1143

QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCCTGCTAATAT 1020
DB 1144 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCCTGCTAATAT 1203

QY 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
DB 1204 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1263

QY 1081 TTCAGTCCACCAAGAAATTTTGTGACTTTCACCTTTTGCAACTGGCAAAATAATTTGGACACAT 1140
DB 1264 TTCAGTCCACCAAGAAATTTTGTGACTTTCACCTTTTGCAACTGGCAAAATAATTTGGACACAT 1323

QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATGACAGCTATTGATCTTAGCAACAAAGCTTC 1200
DB 1324 GCTCAAAATTAAGGGAGACATAGATTCAAAATGACAGCTATTGATCTTAGCAACAAAGCTTC 1383

QY 1201 ATTAGCATTTTACAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
DB 1384 ATTAGCATTTTACAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1443

QY 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGACCAACATTAAACACAAACCAATCAACA 1320
DB 1444 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGACCAACATTAAACACAAACCAATCAACA 1503

QY 1321 CATCATGTTTACAGAACTCTTTCAGGAATA 1348
DB 1504 CATCATGTTTACAGAACTCTTTCAGGAATA 1531

RESULT 4
AY407445 1326 bp DNA linear GSS 15-DEC-2003
LOCUS Homo sapiens PLA2G7 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY407445
VERSION AY407445.1 GI:39763416
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1326)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1326)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source 1..1326
/organism="Homo sapiens"

		/mol_type="genomic DNA" /db_xref="taxon:9606" <1..>1326 /gene="PLA2G7" /locus_tag="HCM2893"	
		ORIGIN	
Query Match		92.2%; Score 1255; DB 9; Length 1326;	
Best Local Similarity		94.8%; Pred. No. 0;	
Matches 1255; Conservative		0; Mismatches 69; Indels 0; Gaps 0;	
QY	38	ATGGTGCACCCAAATGTCATGTGCTTTCTGCTCTGCGGCTGCCTGGCTGTGGTTTAT	97
Db	1	ATGGTGCACCCAAATGTCATGTGCTTTCTGCTCTGCGGCTGCCTGGCTGTGGTTTAT	60
QY	98	CCTTTTGACTGGCAATACATAAATCCTGTTGCCCATPATGAATCAATCAGCATGGGTCAAC	157
Db	61	CCTTTTGACTGGCAATACATAAATCCTGTTGCCCATPATGAATCAATCAGCATGGGTCAAC	120
QY	158	AAATACAAAGTACTGATGGCTGCTGCAAGCTTTGGCAAACTAATAATCCCCGGGAAAT	217
Db	121	AAATACAAAGTACTGATGGCTGCTGCAAGCTTTGGCAAACTAATAATCCCCGGGAAAT	180
QY	218	GGCCTTATTCGGTGTGTACAGACTTAATGTTTGATCACACTAATAAGGGCACTTC	277
Db	181	GGCCTTATTCGGTGTGTACAGACTTAATGTTTGATCACACTAATAAGGGCACTTC	240
QY	278	TTGCGTTTATATTATCCATCCCAAGATAATGATCGCTTGACACCTTTGGATCCCAAT	337
Db	241	TTGCGTTTATATTATCCATCCCAAGATAATGATCGCTTGACACCTTTGGATCCCAAT	300
QY	338	AAAGAAATATTTTGGGCTCTTAGCAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATT	397
Db	301	AAAGAAATATTTTGGGCTCTTAGCAAAATTTCTTGGAAACACACTGGCTTATGGGCAACATT	360
QY	398	TTGAGGTTACTCTTTGGTTCAATGACAACTCCTGCAAACTGGAATTCCTCTGAGGCCT	457
Db	361	TTGAGGTTACTCTTTGGTTCAATGACAACTCCTGCAAACTGGAATTCCTCTGAGGCCT	420
QY	458	GGTGAAAAATATCCACTTGTGTTTCTCATGCTTGGGGCAATTCAGGACATTTAT	517
Db	421	GGTAAAAATATCCACTTGTGTTTCTCATGCTTGGGGCAATTCAGNNNNNNNN	480
QY	518	TCTGCTATTGGCAATTGACCTGGCATCTCATGGGTTTATAGTTGCTGTAGAACACAGA	577
Db	481	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNA	540
QY	578	GATAGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGAC	637
Db	541	GATAGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGAC	600
QY	638	AAGTCTTGGCTCTACCTTAGAACCTTGAAACCAAGAGGAGGAGACACATATACGAAATGAG	697
Db	601	AAGTCTTGGCTCTACCTTAGAACCTTGAAACCAAGAGGAGGAGACACATATACGAAATGAG	660
QY	698	CAGTACGGCAAGAGCAAAAGATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTGAT	757
Db	661	CAGTACGGCAAGAGCAAAAGATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTGAT	720
QY	758	CATGAAAGCCAGTGAAGAATGCATTAGATTTAAAGTTTGATATGGAACAACTGAAGGAC	817
Db	721	CATGAAAGCCAGTGAAGAATGCATTAGATTTAAAGTTTGATATGGAACAACTGAAGGAC	780
QY	818	TCATTATTAGTGGGAAAAAATAGCAGTAATGGACATTCCTTTGGTGGAGCAACGGTTATT	877
Db	781	TCATTATTAGTGGGAAAAAATAGCAGTAATGGACATTCCTTTGGTGGAGCAACGGTTATT	840
QY	878	CAGACTCTTAGTGAAGATCAGAGATTCAGATGTGGTATTGCCCTGGATGCATGATGTTT	937
Db	841	CAGACTCTTAGTGAAGATCAGAGATTCAGATGTGGTATTGCCCTGGATGCATGATGTTT	900
QY	938	CCACTGGGTGATGAAGTATATTCCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAA	997

Db	901	CCACTGGGTGATGAAGTATATTCCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAA	960
QY	998	TATTTCCAAATATCCTGCTAATATCATAAAAATGAAAAATGCTACTCACCTGATAAGAA	1057
Db	961	TATTTCCAAATATCCTGCTAATATCATAAAAATGAAAAATGCTACTCACCTGATAAGAA	1020
QY	1058	AGAAAGATGATTACAATCAGGGTTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCA	1117
Db	1021	AGAAAGATGATTACAATCAGGGTTCAGTCCACCAGAAATTTTGTGCTGACTTCACTTTTGCA	1080
QY	1118	ACTGGCAAAATTAATTGGACACATGCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCT	1177
Db	1081	ACTGGCAAAATTAATTGGACACATGCTCAAAATTAAGGGAGACATAGATTCAAATGCAGCT	1140
QY	1178	ATTGATCTTAGCAACAAAGCTTCAATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAAA	1237
Db	1141	ATTGATCTTAGCAACAAAGCTTCAATTAGCATTTCTTACAAAAGCATTTAGGACTTCATAAA	1200
QY	1238	GATTTTGATCAGTGGGACTGCTTGATTTGAAGGAGATGATGAGAAATCTTATCCAGGACC	1297
Db	1201	GATTTTGATCAGTGGGACTGCTTGATTTGAAGGAGATGATGAGAAATCTTATCCAGGACC	1260
QY	1298	AACATTAACACAAACCAATCAACATCATGTTACAGAACTCTTCAGGAATAGAGAAATAC	1357
Db	1261	AACATTAACACAAACCAATCAACATCATGTTACAGAACTCTTCAGGAATAGAGAAATAC	1320
QY	1358	AATT 1361	
Db	1321	AATT 1324	

RESULT 5
AY407446

LOCUS
DEFINITION
Pan troglodytes PLA2G7 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION
AY407446

VERSION
AY407446.1 GI:39763417

KEYWORDS
GSS.

SOURCE
Pan troglodytes (chimpanzee)

ORGANISM
Pan troglodytes

REFERENCE
AUTHORS
1 (bases 1 to 1326)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 1326)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
source
1. .1326
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1326
/gene="PLA2G7"
/locus_tag="HCM2893"

gene

ORIGIN

Query Match 91.6%; Score 1247; DB 9; Length 1326;


```
QY 469 TCCACTTGTGTTTTTCTCATGGTCTTGGGGCAATTCAGGACACTTTATTTCTGCTATTGG 528
Db 885 TCCACTTGTGTTTTTCTCATGGTCTTGGGGCAATTCAGGACACTTTATTTCTGCTATTGG 826
QY 529 CATTGACCTGGCATCTCATGGGTTTATAGTGTCTGTGTAGAACACAGAGATAGATCTGC 588
Db 825 CATTGCCCTGGCATCTCATGGGTTTATAGTGTCTGTGTAGAACACAGAGATAGATCTGC 766
QY 589 ATCTGCACTTACTATTTCAGGACCAATCTGTCTGCAGAAATAGGGACAAAGTCTTGGCT 648
Db 765 ATCTGCACTTACTATTTCAGGACCAATCTGTCTGCAGAAATAGGGACAAAGTCTTGGCT 706
QY 649 CTACCTTAGAACCTTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCA 708
Db 705 CTACCTTAGAACCTTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCA 646
QY 709 AAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGTATTTGACATTTGATGATGAAAGCC 768
Db 645 AAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGTATTTGACATTTGATGATGAAAGCC 586
QY 769 AGTGAAGATGCATTAGATTAAAGTTTATGATATGGAACAACCTGAAGGACTCTATTGATAG 828
Db 585 AGTGAAGATGCATTAGATTAAAGTTTATGATATGGAACAACCTGAAGGACTCTATTGATAG 526
QY 829 GGAAAAATAGCAGTAATTGGACATCTCTCAGTCTGTGAGCAACGGTTATTGACACTCTTAG 888
Db 525 GGAAAAATAGCAGTAATTGGACATCTCTCAGTCTGTGAGCAACGGTTATTGACACTCTTAG 466
QY 889 TGAAGATCAGAGATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGA 948
Db 465 TGAAGATCAGAGATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGA 406
QY 949 TGAAGTATATCCAGAAATCTCAGCCCTCTTTTATCAACTCTGAAATATTTCCAATA 1008
Db 405 TGAAGTATATCCAGAAATCTCAGCCCTCTGKTTATCAACTCTGAAATATTTCCAATA 346
QY 1009 TCCTGCTAATATCATAAAAATGAAAAATGCTACTCACTGATAAAGAAAGAAAGATGAT 1068
Db 345 TCCTGCTAATATCATAAAAATGAAAAATGCTACTCACTGATAAAGAAAGAAAGATGAT 286
QY 1069 TACAATCAGGGGTTTCAGTCCACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAAT 1128
Db 285 TACAATCAGGGGTTTCAGTCCACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAAT 226
QY 1129 AATTGGACACATGCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAG 1188
Db 225 AATTGGACACATGCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAG 166
QY 1189 CAACAAAGCTTCATTAGCATCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGATCA 1248
Db 165 CAACAAAGCTTCATTAGCATCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGATCA 106
QY 1249 GTGGGACTGCTTGATTGAGGAGATGATGAGAAATCTTATCCAGGGACCAACATTAAACAC 1308
Db 105 GTGGGACTGCTTGATTGAGGAGATGATGAGAAATCTTATCCAGGGACCAACATTAAACAC 46
QY 1309 AACCATCAACACATCATGTTACAGAACTCTTCAGGAATAGAGAA 1353
Db 45 AACCATCAACACATCATGTTACAGAACTCTTCAGGAATAGAGAA 1
```

```
RESULT 7
CR608291
LOCUS CR608291 1158 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1087YO19 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR608291 GI:50489098
VERSION CR608291.1
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1158)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1158
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1087YO19"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
```

```
Query Match 65.3%; Score 888.4; DB 3; Length 1158;
Best Local Similarity 99.9%; Pred. No. 4.1e-232;
Matches 889; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTCCCAACCAATTGCATGT 60
Db 124 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTCCCAACCAATTGCATGT 183
QY 61 GCCTTTCTGCTCTGCGGCTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 184 GCCTTTCTGCTCTGCGGCTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
QY 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAGTACTGATGGCTGC 180
Db 244 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAGTACTGATGGCTGC 303
QY 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATCCGTTGTTGTAC 240
Db 304 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATCCGTTGTTGTAC 363
QY 241 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTCTTGCCTTTATATATCCATCCCA 300
Db 364 AGACTTAATGTTTGTATCACACTAATAAGGGCACCTTCTTGCCTTTATATATCCATCCCA 423
QY 301 AGATAATGATCGCCTTGACACCCCTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 424 AGATAATGATCGCCTTGACACCCCTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 483
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 420
Db 484 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 543
QY 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGGTGAATAATATCCACTTGTGT 480
Db 544 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGGTGAATAATATCCACTTGTGT 603
QY 481 TTTTCTCATGTTCTTGGGGCAATTCAGGACACTTTTATTTCTGCTATTGGCATTGACCTGGC 540
Db 604 TTTTCTCATGTTCTTGGGGCAATTCAGGACACTTTTATTTCTGCTATTGGCATTGACCTGGC 663
QY 541 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTTA 600
Db 664 ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTTA 723
```



```
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAAGTCTTGGCTCTACCTTAGAAC 660
Db 724 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGACAAGTCTTGGCTCTACCTTAGAAC 783
QY 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGACGAGGTACGGCAAGAGCAAAAGA 720
Db 784 CCTGAAACAAGAGGAGGAGACACATATACGAAATGACGAGGTACGGCAAGAGCAAAAGA 843
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTGATGATGATGATGATGATGATGATGATGATGATG 780
Db 844 ATGTTCCCAAGCTCTCAGTCTGATTTGATGATGATGATGATGATGATGATGATGATGATG 903
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGACTCTATTGATAGGGAATAATAGC 840
Db 904 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGACTCTATTGATAGGGAATAATAGC 963
QY 841 AGTAATGGACATCTTTTGGTGGAGCAACGGTTATTAGACTCTTAGTG 890
Db 964 AGTAATGGACATCTTTTGGTGGAGCAACGGTTATTAGACTCTTAGGG 1013

RESULT 8
AL573565/c
LOCUS
DEFINITION
AL573565 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1049YE02 3-PRIME, mRNA sequence.
ACCESSION
AL573565.2 GI:31294910
VERSION
AL573565.2
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 946)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On Feb 16, 2001 this sequence version replaced gi:12932922.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3382.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1049BC01NP1&c=3382.r.
FEATURES
Location/Qualifiers
1..946
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1049YE02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Query Match 64.7%; Score 881; DB 1; Length 946;
Best Local Similarity 93.9%; Pred. No. 4.le-230;
Matches 882; Conservative 28; Mismatches 29; Indels 0; Gaps 0;
QY 410 TTTGGTTCAATGACAACTCTGCAAACTGGAATCCCTCTGAGGCCCTGTGAAAAATAT 469
Db 939 YTTGGTTCAATGACAACTCTGCAAACTGGAATCCCTCTGAGSCCTGTGAAAAATAT 880
QY 470 CCACTTGTTGTTTTTCTCATGGTCTTGGGGCATTCAGGACACTTTATTCTGCTATTGGC 529
```

```
Db 879 CCACTTGTTGTTTTTCTCATGSTCTTGGGCAATTCAGGACACTTTATTCTGCTATTGGC 820
QY 530 ATTGACCTGGCATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCA 589
Db 819 ATTGMCCTGGCATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCA 760
QY 590 TCTGCAACTTACTATTTCAAGSACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTC 649
Db 759 TCTGCAACTTACTATTTCAAGSACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTC 700
QY 650 TACCTTAGAACCTGAAACAGAGAGGAGACACATATACGAAATGAGCAGGTACGGCAA 709
Db 699 TACCTTAGAACCTGAAACAGAGAGGAGACACATATACGAAATGAGCAGGTACGGCAA 640
QY 710 AGAGCAAAAGAGATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTCATGGAAGCCA 769
Db 639 AGAGCAAAAGAGATGCGCCASGCTCTCAGTCTGATTTCTTGACATTCATGGAAGCCA 580
QY 770 GTGAAGAATGCATTAGATTTAAAGTTTGTATGTAAGAACCAACTGAAGGACTCTATTGATAGG 829
Db 579 GTGGAAGAGGCATTAGATGTAAGTKTGATATGGAACCAACTGAAGGACTCTATTGATAGG 520
QY 830 GAAAAAATAGCAGTAATTGGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGT 889
Db 519 GAAAAAATGCRGTAATTGGACAGTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGT 460
QY 890 GAAGATCAGAGATTCAGATGTGGTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGAT 949
Db 459 GAAGATCAGAGATTCAGATGTGGTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGAT 400
QY 950 GAAGTATATTCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCAATAT 1009
Db 399 GAAGTATATTCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCAATAT 340
QY 1010 CCTGCTAATATCAAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATT 1069
Db 339 CCYGCMAATATCATAAAAKGMAAAATGCMACTCMCTGATAAAGAAAGAAAGATGATS 280
QY 1070 ACAATCAGGGGTTTCAGTCCACCAGAAATTTTGTGACTTCACCTTTTGCAACTGGCAAAATA 1129
Db 279 ACAATCAGGGGTTTCAGTCCACCAGAAATTTTGTGACTTCACCTTTTGCAACTGGCAAAATA 220
QY 1130 ATTGGACACATGCTCAAATTAAGGAGAGACATAGATTCAAATGACAGCTATTGATCTTAGC 1189
Db 219 ATTGGACACATGCTCAAATTAAGGAGAGACATAGATTCAAATGACAGCTATTGATCTTAGC 160
QY 1190 AACAAAGCTTCATTAGCATTTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAG 1249
Db 159 AACAAAGCTTCATTAGCATTTCTTAAATKCAATTTAGGACTTCATAATGATTTTGTGTCAG 100
QY 1250 TGGGACTGCTTGATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAAACACA 1309
Db 99 TGGGACTGCTTGATTGAAGGAGATGATGAGAACTTTATTCAGGGGCAACATTAAAYACA 40
QY 1310 ACCAATCAACACATCATGTTTACAGAACTCTTTCAGGAATA 1348
Db 39 ACCAATCAACACCTTCGTGTTACAGAACTCTTTCAGGAATA 1
RESULT 9
AL554852
LOCUS
DEFINITION
AL554852 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1087YO19 5-PRIME, mRNA sequence.
ACCESSION
AL554852
VERSION
AL554852.3 GI:45859601
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1011)
```


JOURNAL REFERENCE AUTHORS	Nature 420, 563-573 (2002) 6 (bases 1 to 1890) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE JOURNAL	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/. Location/Qualifiers 1. .1890 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:D130049018" /db_xref="taxon:10090" /clone="D130049018" /tissue type="spinal ganglion" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="12 days embryo" 372. .1694 /note="unnamed protein product; phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma) (MGD MG1:1351327, GB NM_013737, evidence: BLASTN, 99%, match=1495) putative" /codon_start=1 /protein_id="BAC34647.1" /db_xref="GI:26341970" /translation="MVPLKQLALFCLLCPLPWVHPFHWDTSFDFRPSVMFHLQSVMSAAGSHSKIPKNGSYPVGCTDLFMFGYNESVFLRYPAQDQRLDTWIPNKEYFLGLSIFLGTSPISVGNILHLLYGLTTPASWNSPLRTGEKYPLIVFSGHGLGAFRTIYS AIGIGLASNGFIVATVEHRDSASATYFFEDQVAAKVENRWLYLRKVQEESESVRK EQVQORAI ECSRALSAILDIEHGD PKENVLGS AFDMKOLKDAIDETKIALMGHSFGGA TVLQALSE DORFCR GV ALDPWY PVNEELYSRTLQPLLFINS AKFQTPKDI AKMKKFY QPDKERKMITIKGSVHQNFDDFTFVTGKIIGNKLTJLKGIDSRVAIDLTKNKA SMAFLQ KHLGLQKOFDQDPLVEGDENLIPGSPFDVTVQVPAQQHSPGSGQTQN"
FEATURES source	
CDS	
ORIGIN	
Query Match	59.4%; Score 808.2; DB 3; Length 1890;
Best Local Similarity	75.2%; Pred. No. 4.7e-210;
Matches 1021; Conservative	0; Mismatches 333; Indels 3; Gaps 1;
QY	5 AGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGGCCACCCCAAAATTGCATGTGCTT 64
Db	
QY	65 TTCTGCCTCTGGCGTGCCTGGCTGTGGTTTATCCTTTTGACTGGCAATACATAAATCCT 124
Db	
QY	399 TTCTGCCTCTCTGCTGCTCCCTCCATGGGTCCATCCTTTTTCATCTGGCAAGACACATCTTCT 458
Db	
QY	125 GTTGCCCATATGAAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGCTGCA 184
Db	
QY	459 TTTG---ACTTCAGGCCGTCAGTAATGTTTTCACAAGCTCCAAATCGGTGATGTCTGCTGCC 515
Db	
QY	185 AGCTTTGGCCAAACTAAATCCCGGGGAAATGGCCCTTATTCCTGTTGGTTGTACAGAC 244
Db	
Db	516 GGTCTGTCCTAGTAAATCCCAAGGAAATGGATCGTACCCGTCGGTTGTACAGAT 575
QY	245 TTAATGTTTGATCACACTAATAAGGCACCTTCTTCGCTTTATATATATATCCATCCCAAGAT 304
Db	
Db	576 CTGATGTTTCGGTATGGGAATGAGAGCGTCTTCGTCGCTTTGTACTACCCAGCTCAAGAT 635
QY	305 AATGATCGCTTGACACCTTTTGATCCCAATAAAGAAATATTTTGGGGTCTTTAGCAAA 364
Db	
Db	636 CAAGTCCCTCGACACTGTTTGGATCCCAACAAAGAAATATTTTGGGTCTTAGTATA 695
QY	365 TTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAATGACA 424
Db	
Db	696 TTTCTTGGAAACACCCAGTATTTGTAGGCAATATTTTACACCTCTTATATGTTCTCTGACA 755
QY	425 ACTCTGCAAACTGGAATTCCTCTGAGGCCCTGGTGAATAATATCCACTTGTGTTTTT 484
Db	
Db	756 ACTCTGCAAGCTGGAATTCCTTTGAGGACTGGAGAAAAATACCCACTCATTTGCTTT 815
QY	485 TCTCATGGTCTTTGGGCATTCAGGACACTTTTATTTCTGCTATTGGCAATTGACCTGGCATCT 544
Db	
Db	816 TCTCATGGTCTCGGAGCTTCAGGACGATTTATTTCTGCTATTGGCAATTGCTTGGCATCT 875
QY	545 CATGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCATCTGCAACTTACTAT 604
Db	
Db	876 AATGGGTTTATAGTGGCCACTGTGCAACACAGACAGATCTGCATCGGCAACTTACTTT 935
QY	605 TTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGGCTCTTACCTTAGAACCCCTG 664
Db	
Db	936 TTTGAAGACCCAGGTGGCTGCAAAAGTGGAAAAACAGGTCTTGGCTTTTACCTGAGAAAAAGTA 995
QY	665 AAACAAGAGGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAAGAAATGT 724
Db	
Db	996 AAACAAGAGGAGTCCGAAAGTGTCCGGAAGAACACAGGTTCAGCAAAAGAGCAATAGAAATGT 1055
QY	725 TCCCAAGCTCTCAGTCTGATTCTTGACATTGATCATGGAAGCCAGTGAAGAAATGCATTA 784
Db	
Db	1056 TCCCGGGCTCTCAGTGGGATTTCTTGACATTGGAACATGGAGACCCAAAGAGAATGTACTA 1115
QY	785 GATTTAAAGTTTGATATGGAAACAACCTGAAGGACTCTATTGTAGTGGGAAAAAATAGCAGTA 844
Db	
Db	1116 GGTTCAGCTTTTGACATGAACACAGCTGAAGAGTGTCTATTGTAGAGACTAAAAATAGCTTTG 1175
QY	845 ATTGACATTTCTTTTGGTGAGCAACGGTTTATTTCAGACTCTTTAGTGAAGATCAGAGATTC 904
Db	
Db	1176 ATGGGACATTTCTTTTGGAGGAGCAACAGTTCTTCAAGCCCTTACTGAGGCCAGAGATTC 1235
QY	905 AGATGTGGTATTGCCCTGGATGGATGGATGTTTCCACTGGGTGATGAAGTATATTCCAGA 964
Db	
Db	1236 AGATGTGGAGTTGCTCTTGATCCATGGATGTATCCGGTGAACGAGAGCTGTACTCCAGA 1295
QY	965 ATTCTCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATATA 1024
Db	
Db	1296 ACCCTCCAGCCTCTCTCTTTTATCAACTCTGCCAAATTCAGACTCCAAAGGACATCGCA 1355
QY	1025 AAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTCA 1084
Db	
Db	1356 AAAATGAAAAAAGTTTCTACAGCCCTGACAGGAAAGGAAATGATTACAATCAAGGGCTCA 1415
QY	1085 GTCCACCAAGAAATTTTGCTGACTTCACTTTTGGCAACTGGCAAAATTAATGGACACATGCTC 1144
Db	
Db	1416 GTGCACCAAGAACTTTGACGACTTTTACTTTTGTAACTGGCAAAATTAATGGAAACAAGCTG 1475
QY	1145 AAATTAAGGAGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTCAATTA 1204
Db	
Db	1476 ACACGTGAAAGGAGAAATCGATTCCAGAGTAGCCATCGACCTCACCAACAAAGCTTCGATG 1535
QY	1205 GCATTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATT 1264
Db	

Db 1536 GCTTTCTTACAAAGCATTTAGGGCTTCAGAAAGACTTTGATCAGTGGGACCCCTCTGGTG 1595

QY 1265 GAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACAAACCAATCAACACATC 1324

Db 1596 GAAGGAGATGATGAGAACTGATTCCTGGGTCAACCTTGACCGCAGTCACCCAGGTCGCG 1655

QY 1325 ATGTTACAGAACTCTTCAGGAATAGAGRAATACAATT 1361

Db 1656 GCTCAGCAACACTCTCCAGGATCAGAGACCCAGAAATT 1692

RESULT 11

AK005210

LOCUS

DEFINITION Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500011H20 product:phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma), full insert sequence.

ACCESSION AK005210

VERSION AK005210.1 GI:12837612

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,

TITLE
JOURNAL

Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.jp/) for further details.

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGAGCGGCCGAATTAATTCGAGTTAATAAATATATCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

FEATURES

source

Location/Qualifiers

1..1695

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="FANTOM DB:1500011H20"

/db_xref="taxon:10090"

/clone="1500011H20"

/sex="male"

/tissue_type="cerebellum"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="adult"

165..1487

/note="phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma) (MGD|MGI:1351327, GB|NM_013737, evidence: BLASTN, 99%, match=1495) putative"

misc_feature

ORIGIN

Query Match 57.7%; Score 785.2; DB 3; Length 1695;

Best Local Similarity 75.1%; Pred. No. 9.3e-204;

Matches 1020; Conservative 0; Mismatches 333; Indels 5; Gaps 3;

QY 5 AGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTCCACCCCAATTGCATGTGTT 64

Db 132 ACATCAAACTGAAGCCACTGCTCAGCTCCTAAGATGGTACCACCTCAAACCTGCAGGCGTT 191

QY 65 TTCTGCCTCTGCGGCTGCCTGGCTGTGGTTTATCTTTTGACTGGCAATACATAATCCT 124

Db 192 TTCTGCCTCCTCTGCTGCCTCCCATGGGTCCATCTTTTCACTGGCAAGACACATCTTCT 251

QY 125 GTTCCCCATATGAATCATCAGCATGGGTCAACAAATACAAGTACTGATGGCTGCTGCA 184

Db 252 TTGTG---ACTTCAGGCCGTCAGTAATGTTTTCACAAGTCCAATCGGTGATGTCTGTGCC 308

QY 185 AGCTTTGGCCAAACTAAATCCCCGGGGGAAATGGGCCCTTATTCGTTGGTTGTACAGAC 244

Db 309 GGCTCTGGCCATAGTAAATCCCCAAAGGAATGGATCGTACCCCGTCGGTTGTACAGAT 368

QY 245 TTAATGTTTGATCACACTAATAAGGCACCTTCTTGGCGTTTATATATATCCATCCCAGAT 304

Db 369 CTGATGTTTCGGTTATGGGAATGAGAGCGTCTTCGTGCGTTTGTACTACCCAGCTCAAGAT 428

QY 305 AATGATCGCCTTGACACCCCTTTTGATCCCAATAAAGAAATATTTTGGGGTCTTAGCAAA 364

Db 429 CAAGGTCGCCTCGACACTGTTTGGATCCCAACAAAGAAATATTTTGGGTCTTAGTATA 488

QY 365 TTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAATGACA 424

```
Db 489 TTTCTTGGAAACACCCAGTATTGTAGGCAATATTTACACCTCTATATGTTCTCTGACA 548
Qy 425 ACTCCTGCAAACTGGAATTCCTCTGAGGCTGGTGAATAATCCACTTGTGTTTTT 484
Db 549 ACTCCTGCAAGCTGGAATTCCTCTGAGGACTGGAGAAAATACCCACTCATGTCTTT 608
Qy 485 TCTCATGGTCTTTGGGCATTACAGACACTTTTATTTCTGCTATTGGCATTGACCTGGCATCT 544
Db 609 TCTCATGGTCTCGGAGCCTTCAGGACGATTTATTTCTGCTATTGGCATTGGCTTGGCATCT 668
Qy 545 CATGGTTTATAGTTGCTGCTGTGTAACAACACAGAGATAGATCTGCATCTGCAACTTACTAT 604
Db 669 AATGGGTTTATAGTGGCCACTGTGGAACACAGACAGATCTGCATCGGCAACTTACTTT 728
Qy 605 TTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTTACCTTAGAACCTTG 664
Db 729 TTTGAAGACCAGGTGCTGCAAAAGTGGAACACAGGTCTTGGCTTACCTGAGAAAAGTA 788
Qy 665 AAACAAGAGGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAAAGATG- 723
Db 789 AAACAAGAGGAGTCGGAAAGTGTCCGGACAGAACAGGTTTCAGCAAGAGCAATAGATGA 848
Qy 724 TTCCCAAGCTCTCAGTCTGATTCTTGACATTGATCATGGAAAGCCAGTGAAGATGCATT 783
Db 849 TTCCCGGGCTCTCAGTGGCATACTTGACATTGAACATGGAGACCCCAAAAGAGATGTACT 908
Qy 784 AGATTTAAAGTTTGATATGGAACAACCTGAAGGACTTATTGATAGGGAATAATAGCAGT 843
Db 909 AG-TTTCAGCTTTTGACATGAACACAGCTGAAGGATGCTATTGATGAGACTAAATAGCTTT 967
Qy 844 AATTGACATCTTTTGGTGGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAGATT 903
Db 968 GATGGACATCTTTTGGAGGAGCAACAGTCTTCAAGCCCTTAGTGAGGACCAGAGATT 1027
Qy 904 CAGATGGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAG 963
Db 1028 CAGATGGGAGTTGCTCTTGATCCATGGATGATCCGGTGAACGAGAGCTGTACTCCAG 1087
Qy 964 AATTCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATCAT 1023
Db 1088 AACCTTCAGCCCTCTCCTCTTTATCAACTCTGCCAAATCCAGACTCCAAAGGACATGCG 1147
Qy 1024 AAAAATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTT 1083
Db 1148 AAAAATGAAAAAGTTCTACAGCCTGACAAAGAAAGAAAGATGATTACAATCAAGGCTC 1207
Qy 1084 AGTCCACAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCT 1143
Db 1208 AGTGCAACAGAACTTTGACGACTTTACTTTTGTAACCTGGCAAAATAATTGGAAACAAGCT 1267
Qy 1144 CAAATTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATT 1203
Db 1268 GACACTGAAGGAGAAATCGAATCCAGATAGCCATCGACCTCACCAACAAAGCTTCGAT 1327
Qy 1204 AGCATTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGAT 1263
Db 1328 GGCTTTCTTACAAAAGCAATTTAGGCTTCAGAAAGACTTTTGATCAGTGGGACCCCTCGT 1387
Qy 1264 TGAAGGAGATGATGAGAACTTTATTCAGGACCAACATTAACACAAACCAATCAACACAT 1323
Db 1388 GGAAGGAGATGATGAGAACTGATTCCTGGGTCAACCTTTGACGCGAGTCACCCAGGTCC 1447
Qy 1324 CATGTTACGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1448 GGCTCAGCAACACTCTCCAGGATCACAGACCCAGAAATT 1485
```

RESULT 12
AL552617 1007 bp mRNA linear EST 30-MAR-2004
LOCUS AL552617 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0DI067YM18 5-PRIME, mRNA sequence.

AL552617
AL552617.3 GI:45857398
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1007)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31274432.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3382.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI067BG09QP1&c=3382.r.

Location/Qualifiers
1..1007
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI067YM18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 55.9%; Score 761.2; DB 1; Length 1007;
Best Local Similarity 98.6%; Pred. No. 3.1e-197;
Matches 785; Conservative 3; Mismatches 6; Indels 2; Gaps 2;

```
Qy 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCGATGT 60
Db 209 TGAGAGACTAAGCCGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCCAAATTCGATGT 268
Qy 61 GCTTTTCTGCTCTGCGGCTGCCCTGGCTGTGGTTATCCTTTTGACTGGCAATACATAAA 120
Db 269 GCTTTTCTGCTCTGCGGCTGCCCTGGCTGTGGTTATCCTTTTGACTGGCAATACATAAA 328
Qy 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 180
Db 329 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC 388
Qy 181 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAATGGGCCCTTATCCGTTGGTTGTAC 240
Db 389 TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAATATGGGCCCTTATCCGTTGGTTGTAC 448
Qy 241 AGACTTAAATGTTTGATCACACTAATAAGGGCACTTCTTGGCTTTATATATCCATCCCA 300
Db 449 AGACTTAAATGTTTGATCACACTAATAAGGGCACTTCTTGGCTTTATATATCCATCCCA 508
Qy 301 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 509 AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 568
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 569 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 628
Qy 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGAGGCTGGAATAATCCACTTGTGT 480
Db 629 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGAGGCTGGAATAATCCACTTGTGT 688
```


Thu Mar 17 08:25:04 2005

QY 758 CATGGAAGCCAGTGAAGATGCATTAGATTAAAGTTTGTATATGAACCAACTGAAGGAC 817
Db 721 CATGGAGACCCAAAAGAGAAATGTAAGTTTGTATATGAACCAACTGAAGGAT 780
QY 818 TCTATTGATAGGAAAAAATAGCAGTAATTTGGAGCATTTCTTTGGTGGAGCAACGGTTATT 877
Db 781 GCTATTGATGAGACTAAATAGCTTTGATGGGACATTTCTTTGGAGGAGCAACAGTTCTT 840
QY 878 CAGACTCTTAGTGAAGATCAGAGATTCAGATGTGGTATTGCTTCCCTGGATGCATGGATGTTT 937
Db 841 CAAGCCCTTAGTGGAGACCCAGAGATTCAGATGTGGAGTTGCTTCTTGATCCATGGATGAT 900
QY 938 CCACCTGGGTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAA 997
Db 901 CCGGTGAACGAAGAGCTGTACTCCAGAACCTCCAGCTCTCTCTTATCAACTCTGCC 960
QY 998 TATTTCGAATATCTGCTAATATATCAATAAATAATGAATAATGCTACTCACCTGATAAGAA 1057
Db 961 AAATTCAGACTCCAAAGGACATCGCAAAATGAAAGAGTTCTACCGAGCTGACAAGGAA 1020
QY 1058 AGAAGATGATTACATCAGGGGTTCACTCCAGCAATTTTGTGCTGCTTCACTTTTGCA 1117
Db 1021 AGGAATGATTACATCAAGGGCTCAGTGCCAGCAACTTTGACGACTTTACTTTTGT 1080
QY 1118 ACTGGCAAAATAATGGACACATGCTCAAAATTAAGGGAGACATAGATTCAAAATGCAGCT 1177
Db 1081 ACTGGCAAAATAATGGAAACAAGCTGACACTGAAAGAGAAATCGATTCCAGAGTAGCC 1140
QY 1178 ATTGATCTTAGCAACAAAGCTTCAATTAGCAATTTTACAAAGCAATTTAGGACTTCATAA 1237
Db 1141 ATCGACCTCACCAACAAAGCTTCGATGGCTTTCTTACAAAGCAATTTAGGGCTTCAGAA 1200
QY 1238 GATTTGATCAGTGGGACTGCTTGTATTGAAGGAGATGATGAGAAATCTTATTCAGGGACC 1297
Db 1201 GACTTTGATCAGTGGGACCTCTGTTGGAAGGAGATGATGAGAAATCTGATTCCTGGTCA 1260
QY 1298 AACATTAAACAAACCAATCAACATCATGTTACAGAACTTTCAGGAATAGAGAAATAC 1357
Db 1261 CCCTTTGACGAGTCAACCCAGGCCCGGCTCAGCAACACTCTCCAGGATCAGACCCAG 1320
QY 1358 AATT 1361
Db 1321 AATT 1324

RESULT 15
CA312081/c
LOCUS
DEFINITION
UI-CF-FN0-afj-b-19-0-UI.s1 UI-CF-FN0 Homo sapiens cdna clone
UI-CF-FN0-afj-b-19-0-UI 3', mRNA sequence.
ACCESSION
CA312081
VERSION
CA312081.1 GI:24530179
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 734)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cdna Library preparation: Dr. M. Bento Soares, University of Iowa

14671302
2 (bases 1 to 1326)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..1326
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1326
/gene="PLA2G7"
/locus_tag="HCM2893"
ORIGIN
Query Match 54.2%; Score 738.2; DB 9; Length 1326;
Best Local Similarity 70.4%; Pred. No. 6.8e-191;
Matches 932; Conservative 0; Mismatches 392; Indels 0; Gaps 0;
QY 38 ATGGTGCCACCAAAATTGCATGTGCTTTCTGCTCTCTGCGGTGCTGCTGCTGCTTTAT 97
Db 1 ATGGTACCACTCAAACTGACGGGCTTTCTGCTCTCTGCTGCTCTCCCATGGGTCCAT 60
QY 98 CTTTGTGACTGGCAATACATAAATCTGTTGCCCATATGAATCATCAGCATGGGTCAAC 157
Db 61 CTTTGTGACTGGCAAGACACATCTTTTGTGACTTCAGGCCGCTCAGGTATATGTTTTCAC 120
QY 158 AAAATACAAAGTACTGATGGCTGCTGCAAGCTTTGGCCAAACCTAAATCCCCCGGGAAAT 217
Db 121 AAGCTCCAATCGGTGATGTCTGCTGCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 218 GGGCTTATTCGGTGGTGTACAGACTTAATGTTGTATCAGACTTAATAAGGGCACCTTC 277
Db 181 GGATCGTACCCCGTGGTGTGACAGATCTGATGTCGGTTATGGGAATGAGAGCGTCTTC 240
QY 278 TTGCGTTATATATCCATCCCAAGATAATGATCGCTTGACACCCCTTTGGATCCCAAT 337
Db 241 GTGCGTTGTACTACCCAGCTCAAGATCAAGTTCGGCTGACACTGTTTGGATCCCAAC 300
QY 338 AAAGAAATATTTTGGGTCTTAGCAAAATTTCTTGGAAACACACTGGCTTATGGCAACATT 397
Db 301 AAAGAAATATTTTGGGTCTTAGTATATTTCTTGGAAACACCCAGTATGTAGGCAATAT 360
QY 398 TTGAGGTACTCTTTGGTCAATGACAACTCCTGCAAACTGGAATTTCCCTCTGAGGCT 457
Db 361 TTACACCTCTTATATGTTCTCTGACAACTCCTGCAAGTGAATTTCTCTTAAGGACT 420
QY 458 GGTGAAAAATATCCACTGTTGTTTCTTCTCATGTTCTTGGGGCATTCAGGACACTTTAT 517
Db 421 GGAGAAAAATATACCCGCTCATGTTCTTTCTCATGTTCTGAGGCTTCAGNNNNNNNNN 480
QY 518 TCTGCTATTGGCATTGACCTGGCATCTCATGGTTTATAGTTGCTGTAGAACACAGA 577
Db 481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNA 540
QY 578 GATAGATCTGCATCTGCAACTTACTATTTCAGGACCAATCTGCTGCAGAAATAGGGGAC 637
Db 541 GACAGATCTGCATCGGCAACTTACTTTTGAAGACCCAGGTGGCTGCAAAAGTGGAAAC 600
QY 638 AAGTCTTGGCTCTACCTTAGAACCTTGAAACAGAGGAGGAGACACATATACGAATGAG 697
Db 601 AGGTCTTGGCTTTACCTTGAGAAAAAGTAAACAGAGGAGTCCGAAAGTGTCCGAAAGAA 660
QY 698 CAGGTACGGCAAGAGCAAAAGATGTTCCCAAGCTCTCAGTCTGATTCTTGACATTGAT 757
Db 661 CAGGTTACGCAAGAGCAATAGAAATGTTCCCGGGCTCTCAGTGGGCTCTCAGTGGATTCTTGACATTGAA 720

cdNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cdNA
sequence: 1-24, >AT-rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES

source
1. .734
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-afj-b-19-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-FNO is a subtraced cdNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI) The library was subtraced according to according to
Bonardo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match 50.9%; Score 692.4; DB 6; Length 734;
Best Local Similarity 99.6%; Pred. No. 2.1e-178;
Matches 693; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 666 AACAGAGGAGGAGACATATACGAATGAGCAGGTACGGCAAGACCAAAAGATGTT 725
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
734 AACAGAGGAGGAGACATNTACGAATGAGCAGGTACGCNAAAGACCAAAAGATGTT 675
QY 726 CCCAAGCTCTCAGTCTGATTTCTTGACATTGATCATGGAAAGCCAGTGAAGAATGCATTAG 785
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
674 CCCAAGCTCTCAGTCTGATTTCTTGACATTGATCATGGAAAGCCAGTGAAGAATGCATTAG 615
QY 786 ATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAAAAAATAGCAGTAA 845
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
614 ATTTAAAGTTTGATATGGAACAACCTGAAGGACTCTATTGATAGGGAAAAAATAGCAGTAA 555
QY 846 TTGGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCA 905
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
554 TTGGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCA 495
QY 906 GATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAA 965
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
494 GATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAA 435
QY 966 TTCTTCAGCCCTCTTTTATCACTCTGAATATTTCCAATATCTCGCTAATATCATAA 1025
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
434 TTCTTCAGCCCTCTTTTATCACTCTGAATATTTCCAATATCTCGCTAATATCATAA 375
QY 1026 AAATGAAAAAATGCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGTTTCAG 1085
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
374 AAATGAAAAAATGCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGTTTCAG 315
QY 1086 TCCACAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAAATAATTGGACACATGCTCA 1145
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
314 TCCACAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAAATAATTGGACACATGCTCA 255
QY 1146 AATTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAAAAGCTTCATTAG 1205
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
254 AATTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAAAAGCTTCATTAG 195
QY 1206 CATTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTG 1265
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 194 CATTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTTCATCAGTGGGACTGCTTGATTG 135
QY 1266 AAGGAGATGATGAGAATCTTTATCCAGGACCAACATTAACACAACCAATCAACACATCA 1325
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
134 AAGGAGATGATGAGAATCTTTATCCAGGACCAACATTAACACAACCAATCAACACATCA 75
QY 1326 TGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
74 TGTTACAGAACTCTTTCAGGAATAGAGAAATACAATT 39

Search completed: March 15, 2005, 18:21:44
Job time : 5506.71 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:21 ; Search time 2455.96 Seconds
(without alignments)
10141.035 Million cell updates/sec

Title: US-09-922-067F-9_COPY_848_1361
Perfect score: 514
Sequence: 1 ggacattcttttggaggc.....aggaatagagaatacaatt 514

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514	100.0	1361	6 A41956	A41956 Sequence 9
2	514	100.0	1361	6 AR080658	AR080658 Sequence
3	514	100.0	1361	6 AR084987	AR084987 Sequence
4	514	100.0	1361	6 AR125358	AR125358 Sequence
5	514	100.0	1361	6 BD242703	BD242703 Method fo
6	514	100.0	1361	6 AR205614	AR205614 Sequence
7	514	100.0	1361	6 AX006795	AX006795 Sequence
8	514	100.0	1505	6 CQ717247	CQ717247 Sequence
9	514	100.0	1554	9 BC038452	BC038452 Homo sapi
10	514	100.0	1561	6 AX335487	AX335487 Sequence
11	514	100.0	1561	9 HSU24577	U24577 Human LDL-p
12	512.4	99.7	1335	6 A81400	A81400 Sequence 30
13	512.4	99.7	1335	6 AR064425	AR064425 Sequence
14	512.4	99.7	1335	6 AR083776	AR083776 Sequence
15	512.4	99.7	1335	6 AR141171	AR141171 Sequence
16	512.4	99.7	1335	6 AR142524	AR142524 Sequence
17	512.4	99.7	1335	6 I60383	I60383 Sequence 30
18	512.4	99.7	1505	9 HSU20157	U20157 Human plate
19	512.4	99.7	1520	6 A81377	A81377 Sequence 7

20	512.4	99.7	1520	6 AR064404	AR064404 Sequence
21	512.4	99.7	1520	6 AR083755	AR083755 Sequence
22	512.4	99.7	1520	6 AR141150	AR141150 Sequence
23	512.4	99.7	1520	6 AR142503	AR142503 Sequence
24	512.4	99.7	1520	6 I23385	I23385 Sequence 7
25	512.4	99.7	1520	6 I49901	I49901 Sequence 7
26	512.4	99.7	1520	6 I60362	I60362 Sequence 7
27	512.4	99.7	1520	6 I85595	I85595 Sequence 7
28	509.2	99.1	572	6 A41955	A41955 Sequence 8
29	509.2	99.1	572	6 AR080657	AR080657 Sequence
30	509.2	99.1	572	6 AR084986	AR084986 Sequence
31	509.2	99.1	572	6 AR125357	AR125357 Sequence
32	509.2	99.1	572	6 AR205613	AR205613 Sequence
33	509.2	99.1	572	6 AX006794	AX006794 Sequence
34	403.6	78.5	2191	6 A81392	A81392 Sequence 22
35	403.6	78.5	2191	6 AR064418	AR064418 Sequence
36	403.6	78.5	2191	6 AR083769	AR083769 Sequence
37	403.6	78.5	2191	6 AR141164	AR141164 Sequence
38	403.6	78.5	2191	6 AR142517	AR142517 Sequence
39	403.6	78.5	2191	6 I49915	I49915 Sequence 22
40	403.6	78.5	2191	6 I60376	I60376 Sequence 22
41	403.6	78.5	2191	6 I85609	I85609 Sequence 22
42	403.6	78.5	2222	4 CFU34246	U34246 Dog plasma
43	402	78.2	1506	4 BTU34247	U34247 Bovine plas
44	402	78.2	1533	6 A81393	A81393 Sequence 23
45	402	78.2	1533	6 AR064419	AR064419 Sequence

ALIGNMENTS

RESULT 1
A41956
LOCUS A41956 1361 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 9 from Patent WO9500649.
ACCESSION A41956
VERSION A41956.1 GI:2297493
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1361)
AUTHORS Macphee,C.H., Tew,D.G., Southan,C.D., Hickey,D.M., Gloger,I.S., Lawrence,G.M. and Rice,S.Q.
TITLE LIPOPROTEIN ASSOCIATED PHOSPHOLIPASE A 2?, INHIBITORS THEREOF AND USE OF THE SAME IN DIAGNOSIS AND THERAPY
JOURNAL Patent: WO 9500649-A 9 05-JAN-1995;
COMMENT SMITHKLINE BEECHAM PLC (GB)
FEATURES Other publication JP 8500740T 960130.
source Location/Qualifiers
1..1361
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
38..>1361
/note="unnamed protein product"
/codon_start=1
/protein_id="CAA02638.1"
/db_xref="GI:2297494"
/translation="MVPPKGLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWNKIQV LMAAASFGQTKIPRGNGPYSGCTDLMFDTNKGTLRLYYPSQNDRLDTLWIPNKE YFWGLSKFLGTHWLMGNILRLFLGSMTPANWNSPLRPGEKYPVVFSGHGLGAFRTLY SAIGIDLASHGFIVAVEHRDRSASATYYFKDQSAEIGDKSWLYLRTLKQEEETHIR NEQVRQRAKESQALSILIDIDHGKPVKNALDLKFDMEQLKOSIDREKIAVIGHSFGG ATVIQTLSEDRFCRGIALDAMFFPLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKC YSPDKERKMITIRGSHVQNFADTFATGKIIGHMLKLKGDIDSNAAIDLNSKASLAFI QKHLGLHKDFDQDWCLIEGDDENLIPGTNINTNQHIMLQNSSGIEKYN"

ORIGIN

Query Match 100.0%; Score 514; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
|||||
Db 848 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 907
QY 61 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
|||||
Db 908 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967
QY 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA 180
|||||
Db 968 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA 1027
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
|||||
Db 1028 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
|||||
Db 1088 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1147
QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAACCAATCAACATCATG 360
|||||
Db 1148 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAACCAATCAACATCATG 1207
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1267
QY 421 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAACCAATCAACATCATG 480
Db 1268 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAACCAATCAACATCATG 1327
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 2
AR080658
LOCUS AR080658 1361 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 9 from patent US 5968818.
ACCESSION AR080658
VERSION AR080658.1 GI:10007388
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1361)
AUTHORS Gloger, I.Simon., Lawrence, G.Mark.Prouse. and Rice, S.Quentyn.John.
TITLE Lipoprotein associated phospholipase A2, inhibitors thereof and use of the same in diagnosis and therapy
JOURNAL Patent: US 5968818-A 9 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..1361
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 514; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 848 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 907
QY 61 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 908 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967
QY 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA 180
Db 968 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA 1027

QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1028 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1088 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1147
QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAACCAATCAACATCATG 360
Db 1148 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAACCAATCAACATCATG 1207
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1267
QY 421 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAACCAATCAACATCATG 480
Db 1268 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAACCAATCAACATCATG 1327
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
RESULT 3
AR084987
LOCUS AR084987 1361 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 9 from patent US 5981252.
ACCESSION AR084987
VERSION AR084987.1 GI:10011758
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1361)
AUTHORS MacPhee, C.Houston. and Tew, D.Graham.
TITLE Lipoprotein associated phospholipase A.sub.2, inhibitors thereof and use of the same in diagnosis and therapy
JOURNAL Patent: US 5981252-A 9 09-NOV-1999;
FEATURES Location/Qualifiers
source 1..1361
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 514; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 848 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 907
QY 61 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 908 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967
QY 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA 180
Db 968 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA 1027
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1028 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1088 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1147
QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAACCAATCAACATCATG 360

Db 1148 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207

QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCACTGGGACTGCTTGATTGAA 420

Db 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCACTGGGACTGCTTGATTGAA 1267

QY 421 GGAGATGATGAGAATCTTATCCAGGGACCAACATTAACACAACCAATCAACACATCATG 480

Db 1268 GGAGATGATGAGAATCTTATCCAGGGACCAACATTAACACAACCAATCAACACATCATG 1327

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514

Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 4

LOCUS ARI25358 1361 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 9 from patent US 6177257.

ACCESSION ARI25358

VERSION ARI25358.1 GI:14111420

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1361)

AUTHORS Macphree,C.Houston., Tew,D.Graham., Southan,C.Donald., Hickey,D.Mary.Bernadette., Gloger,I.Simon., Lawrence,G.Mark.Prouse. and Rice,S.Quentyn.John.

TITLE Lipoprotein associated phospholipase A2, inhibitors thereof and use of the same in diagnosis and therapy

JOURNAL Patent: US 617257-A 9 23-JAN-2001;

FEATURES Location/Qualifiers

source 1. .1361

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 514; DB 6; Length 1361;

Best Local Similarity 100.0%; Pred. No. 1.6e-106;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60

Db 848 GGACATTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 907

QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120

Db 908 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 967

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATATCATATAAA 180

Db 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATATCATATAAA 1027

QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240

Db 1028 ATGAAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087

QY 241 CACCAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACATGCTCAA 300

Db 1088 CACCAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACATGCTCAA 1147

QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360

Db 1148 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207

QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCACTGGGACTGCTTGATTGAA 420

Db 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCACTGGGACTGCTTGATTGAA 1267

QY 421 GGAGATGATGAGAATCTTATCCAGGGACCAACATTAACACAACCAATCAACACATCATG 480

Db 1268 GGAGATGATGAGAATCTTATCCAGGGACCAACATTAACACAACCAATCAACACATCATG 1327

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514

Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 5

BD242703 1361 bp DNA linear PAT 17-JUL-2003

LOCUS

DEFINITION Method for purifying low-density lipoprotein-associated phospholipase A2 using immobilized metal affinity chromatography.

ACCESSION BD242703

VERSION BD242703.1 GI:33052473

KEYWORDS JP 2002528084-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1361)

AUTHORS Boyd,H. and Tew,D.G.

TITLE Method for purifying low-density lipoprotein-associated phospholipase A2 using immobilized metal affinity chromatography

JOURNAL Patent: JP 2002528084-A 1 03-SEP-2002;

SMITHKLINE BEECHAM PLC

COMMENT OS Homo sapiens (human)

PN JP 2002528084-A/1

PD 03-SEP-2002

PF 27-OCT-1999 JP 2000578462

PR 28-OCT-1998 GB 9823647.4,28-OCT-1998 GB 9823648.2 PI HELEN BOYD,DAVID GRAHAM TEW

PC C12N15/09,A61P29/00,C07K1/22,C12N5/10,C12N9/16//A61K38/46, PC C12N15/00,

PC C12N5/00,A61K37/54

CC Method for purifying low-density lipoprotein-associated CC phospholipase A2

CC using immobilized metal affinity chromatography FH. Key Location/Qualifiers

FT source 1. .1361

FT Location/Qualifiers

source 1. .1361

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 514; DB 6; Length 1361;

Best Local Similarity 100.0%; Pred. No. 1.6e-106;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60

Db 848 GGACATTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 907

QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120

Db 908 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 967

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATATCATATAAA 180

Db 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATATCATATAAA 1027

QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240

Db 1028 ATGAAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087

QY 241 CACCAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACATGCTCAA 300

Db 1088 CACCAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACATGCTCAA 1147

QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360

Db 1148 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207

QY 361 TTCTTACAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
|||||
Db 1208 TTCTTACAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1267
|||||
QY 421 GGAGATGATGAGAATCTTTATCCAGGAGCAACATTAACACAACCAATCAACACATCATG 480
|||||
Db 1268 GGAGATGATGAGAATCTTTATCCAGGAGCAACATTAACACAACCAATCAACACATCATG 1327
|||||
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
|||||
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
|||||
RESULT 6
AR205614
LOCUS AR205614 1361 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 9 from patent US 6369045.
ACCESSION AR205614
VERSION AR205614.1 GI:21503242
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1361)
AUTHORS Macphree,C.Houston., Tew,D.Graham. and Hickey,D.Mary.Bernadette.
TITLE Phospholipase A2 inhibitors thereof and use of same in diagnosis and therapy
JOURNAL Patent: US 6369045-A 9 09-APR-2002;
FEATURES Location/Qualifiers
source 1. .1361
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 514; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATCTCTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
|||||
Db 848 GGACATCTCTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 907
|||||
QY 61 TGTGGTATGCCCCCTGGATGGATGATGTTCCACTGGGTGATGAAGTATATCCAGAATT 120
|||||
Db 908 TGTGGTATGCCCCCTGGATGGATGATGTTCCACTGGGTGATGAAGTATATCCAGAATT 967
|||||
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
|||||
Db 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 1027
|||||
QY 181 ATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
|||||
Db 1028 ATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087
|||||
QY 241 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
|||||
Db 1088 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1147
|||||
QY 301 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
|||||
Db 1148 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1207
|||||
QY 361 TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
|||||
Db 1208 TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1267
|||||
QY 421 GGAGATGATGAGAATCTTTATCCAGGAGCAACATTAACACAACCAATCAACACATCATG 480
|||||
Db 1268 GGAGATGATGAGAATCTTTATCCAGGAGCAACATTAACACAACCAATCAACACATCATG 1327
|||||
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
|||||

Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
|||||
RESULT 7
AX006795
LOCUS AX006795 1361 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 9 from Patent EP0974663.
ACCESSION AX006795
VERSION AX006795.1 GI:9994827
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Gloger,I.S., Hickey,D.M., Macphree,C.H., Southan,C.D.,
Lawrence,G.M., Rice,S.Q. and Tew,D.G.
TITLE Lipoprotein associated phospholipase a2, inhibitors thereof and use of same in diagnosis and therapy
JOURNAL Patent: EP 0974663-A 9 26-JAN-2000;
SMITHKLINE BEECHAM PLC (GB)
FEATURES Location/Qualifiers
source 1. .1361
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 514; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATCTCTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
|||||
Db 848 GGACATCTCTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 907
|||||
QY 61 TGTGGTATGCCCCCTGGATGCATGGATGTTCCACTGGGTGATGAAGTATATCCAGAATT 120
|||||
Db 908 TGTGGTATGCCCCCTGGATGCATGGATGTTCCACTGGGTGATGAAGTATATCCAGAATT 967
|||||
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
|||||
Db 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 1027
|||||
QY 181 ATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
|||||
Db 1028 ATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087
|||||
QY 241 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
|||||
Db 1088 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1147
|||||
QY 301 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
|||||
Db 1148 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1207
|||||
QY 361 TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
|||||
Db 1208 TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1267
|||||
QY 421 GGAGATGATGAGAATCTTTATCCAGGAGCAACATTAACACAACCAATCAACACATCATG 480
|||||
Db 1268 GGAGATGATGAGAATCTTTATCCAGGAGCAACATTAACACAACCAATCAACACATCATG 1327
|||||
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
|||||
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
|||||

RESULT 8
CQ717247
LOCUS CQ717247 1505 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 3181 from Patent WO02068579.

ACCESSION CQ717247
VERSION CQ717247.1 GI:42278104
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
AUTHORS Kits, such as nucleic acid arrays, comprising a majority of
TITLE humanexons or transcripts, for detecting expression and other uses
JOURNAL Patent: WO 02068579-A 3181 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
source 1..1505
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 514; DB 6; Length 1505;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db |||||
972 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 1031
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db |||||
1032 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA 180
Db |||||
1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA 1151
QY 181 ATGAAAAAATGCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGTTCAGTC 240
Db |||||
1152 ATGAAAAAATGCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGTTCAGTC 1211
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATATTTGGACACATGCTCAA 300
Db |||||
1212 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATATTTGGACACATGCTCAA 1271
QY 301 TTAAAGGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db |||||
1272 TTAAAGGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1331
QY 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTATGATCAGTGGGACTGCTTGATTGAA 420
Db |||||
1332 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTATGATCAGTGGGACTGCTTGATTGAA 1391
QY 421 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACACCAATCAACACATCATG 480
Db |||||
1392 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACACCAATCAACACATCATG 1451
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
Db |||||
1452 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1485
RESULT 9
BC038452
LOCUS BC038452 1554 bp mRNA linear PRI 07-OCT-2003
DEFINITION Homo sapiens phospholipase A2, group VII (platelet-activating
factor acetylhydrolase, plasma), mRNA (cdna clone MGC:46165
IMAGE:5216829), complete cds.
ACCESSION BC038452
VERSION BC038452.1 GI:23512330
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1554)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1554)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgueon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov
Series: IRAC Plate: 78 Row: g Column: 17
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4826883.
FEATURES Location/Qualifiers
source 1..1554
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:46165 IMAGE:5216829"
/tissue_type="Blood, adult leukocytes"
/clone_lib="NIH MGC_118"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
1..1554
/gene="PLA2G7"
/note="synonyms: PAFAH, LDL-PLA2"
/db_xref="LocusID:7941"
/db_xref="MIM:601690"
gene

CDS
179..1504
/gene="PLA2G7"
/codon_start=1
/product="PLA2G7 protein"
/protein_id="AAH38452.1"
/db_xref="GI:23512331"
/db_xref="LocusID:7941"
/db_xref="MIM:601690"
/translation="MVPPKLVFLCLCGLAVVYPFDWQYINVAHMKSSAWVNKIQV
LMAASFQGTQKIPRNGPYSVGCTDLMFDTNKGTFRLRYYPQDNDRDLDITLWPNKE
YFGLSKFLGTHLMGNILRLLEGSMTTPANWNSPLRPGEXPLVVFESHGLGAFRTLY
SAIGIDLASHGFIVAAVEHRDRSASATYFQDSAAEIGKSWLYLRTLKQEEETHIR
NEQVRQAKESQALSLILDIDHGKPVKNALDLKDFDMEQLKDSIDREKIAVIGHSFGG
ATVIQTLEDQRFRCGIALDAMNFPPLGDEVYSRIPQPLFFINSEYFQYPANIKMKKC
YSPDKERKMITIRGVSVHONFADEFTATGKIIGHMLKLKGDIDNSAAIDLSNKASLAFL
QKHLGLHKDFDQWDCLIEGDDENLIPGTNINTNQHIMLQNSSGIEKYN"
320..1426
/gene="PLA2G7"
/note="PAF-AH p_II; Region: Platelet-activating factor
acetylhydrolase, plasma/intracellular isoform II.
Platelet-activating factor acetylhydrolase (PAF-AH) is a
subfamily of phospholipases A2, responsible for
inactivation of platelet-activating factor through
cleavage of an acetyl group. Three known PAF-AHs are the
brain heterotrimeric PAF-AH Ib, whose catalytic beta and
gamma subunits are aligned in pfam02266, the
extracellular, plasma PAF-AH (pPAF-AH), and the
intracellular PAF-AH isoform II (PAF-AH II). This family
aligns pPAF-AH and PAF-AH II, whose similarity was
previously noted"
/db_xref="CDD:pfam03403"

ORIGIN
Query Match 100.0%; Score 514; DB 9; Length 1554;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTTCAGA 60
Db 989 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTTCAGA 1048
Qy 61 TGTGGTATTGCCCTGGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1049 TGTGGTATTGCCCTGGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1108
Qy 121 CCTCAGCCCTCTTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
Db 1109 CCTCAGCCCTCTTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 1168
Qy 181 ATGAAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1169 ATGAAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1228
Qy 241 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1229 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1288
Qy 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db 1289 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1348
Qy 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTTGATTGAA 420
Db 1349 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTTGATTGAA 1408
Qy 421 GGAGATGATGAGAATCTTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 480
Db 1409 GGAGATGATGAGAATCTTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 1468
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1469 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1502

RESULT 10
AX335487
LOCUS
DEFINITION
AX335487
ACCESSION
AX335487.1
GI:18126206
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS
Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D.R. and Weaver, Z.
TITLE
Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL
Patent: WO 0194629-A 5996 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
Location/Qualifiers
source
1..1561
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 100.0%; Score 514; DB 6; Length 1561;
Best Local Similarity 100.0%; Pred. No. 1.6e-106;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTTCAGA 60
Db 1027 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTTCAGA 1086
Qy 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1087 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1146
Qy 121 CCTCAGCCCTCTTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
Db 1147 CCTCAGCCCTCTTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 1206
Qy 181 ATGAAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1207 ATGAAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1266
Qy 241 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1267 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1326
Qy 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db 1327 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1386
Qy 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTTGATTGAA 420
Db 1387 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTTGATTGAA 1446
Qy 421 GGAGATGATGAGAATCTTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 480
Db 1447 GGAGATGATGAGAATCTTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 1506
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1507 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1540

RESULT 11
HSU24577
LOCUS
DEFINITION
U24577
ACCESSION
U24577.1
GI:1314245
HSU24577
Human LDL-phospholipase A2 mRNA, complete cds.
linear
PRI 24-JUL-1996

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1561)

AUTHORS Tew,D.G., Southan,C., Rice,S.Q., Lawrence,M.P., Li,H., Boyd,H.F., Moores,K., Gloger,I.S. and Macphree,C.H.

TITLE Purification, properties, sequencing, and cloning of a lipoprotein-associated, serine-dependent phospholipase involved in the oxidative modification of low-density lipoproteins

JOURNAL Arterioscler. Thromb. Vasc. Biol. 16 (4), 591-599 (1996)

MEDLINE 96197208

PUBMED 8624782

REFERENCE 2 (bases 1 to 1561)

AUTHORS Rice,S.Q.J.

TITLE Direct Submission

JOURNAL Submitted (10-APR-1995) Simon Q.J. Rice, SmithKline Beecham Pharmaceuticals, New Frontiers Science Park North, Third Avenue, Harlow, Essex CM195AW, UK

COMMENT On May 16, 1996 this sequence version replaced gi:790655.

FEATURES Location/Qualifiers

source 1..1561

organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

chromosome="6"

cell_type="T cell"

tissue_type="lymphoma"

dev_stage="adult"

217..1542

function="oxidized modification of low density lipoprotein"

note="PAF-acetylhydrolase"

codon start=1

product="LDL-phospholipase A2"

protein_id="AAB04170.1"

db_xref="GI:1314246"

translation="MVPKLVFLCGLAVVYFPDQWYINPVAHMKSSAWNKIQV LMAASFQTKIPRNGPYSVCGTDLMPDHTNKGTLRLYPSQDNDRLDTLWPNKE YFGLSKFLGTHWLMGNILRLFGSMTPANWNSPLRPGKEYPLVVFSGHGLGAPRTLY SAIGIDLASHGFIVAAVEHRDRSASATYFQDSAAEIGKSWLYLRTLKQEEETHIR NEQVRQRAKESQALSILIDIDHGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSFGG ATVIQTLSQDRFCGIALDWMFPLGDEVYSRIPOPLFFINSEYFOYPANIKMKKC YSPDKERKMITIRGSHQNFADFTPATGKIIGHMLKLKGDIDSNAAIDLSNKASLAFL QKHLGLHKDFDQWDCLEIGDDENLIPGTNINTNQHIMLQNSSGIEKYN"

813..828

note="encodes lipase motif"

1561

note="18 A nucleotides"

misc_feature

polyA_site

ORIGIN

Query Match 100.0%; Score 514; DB 9; Length 1561;

Best Local Similarity 100.0%; Pred. No. 1.6e-106;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATTCCTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60

Db 1027 GGACATTCCTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 1086

Qy 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120

Db 1087 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 1146

Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 180

Db 1147 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 1206

Qy 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 240

Db 1207 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 1266

Qy 241 CACCAGAAATTTTGCTGACTTTCAGCTTTTGCAACTGGGCAAAATAATTGGACACATGCTCAA 300

Db 1267 CACCAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAA 1326

Qy 301 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360

Db 1327 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1386

Qy 361 TTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420

Db 1387 TTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1446

Qy 421 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 480

Db 1447 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 1506

Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514

Db 1507 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1540

RESULT 12

A81400

LOCUS A81400 1335 bp DNA linear PAT 21-JAN-2000

DEFINITION Sequence 30 from Patent WO9909147.

ACCESSION A81400

VERSION A81400.1 GI:6731720

KEYWORDS unidentified

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1335)

AUTHORS Eberhardt,C.D. and Gray,P.

TITLE TRUNCATED PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE

JOURNAL Patent: WO 9909147-A 30 25-FEB-1999;

ICOS CORP (US)

FEATURES Location/Qualifiers

source 1..1335

organism="unidentified"

mol_type="unassigned DNA"

db_xref="taxon:32644"

ORIGIN

Query Match 99.7%; Score 512.4; DB 6; Length 1335;

Best Local Similarity 99.8%; Pred. No. 3.8e-106;

Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATTCCTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60

Db 811 GGACATTCCTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870

Qy 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120

Db 871 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 930

Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAA 180

Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAA 990

Qy 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 240

Db 991 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 1050

Qy 241 CACCAGAAATTTTGCTGACTTTCAGCTTTTGCAACTGGGCAAAATAATTGGACACATGCTCAA 300

Db 1051 CACCAGAAATTTTGCTGACTTTCAGCTTTTGCAACTGGGCAAAATAATTGGACACATGCTCAA 1110

Qy 301 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360

Db 1111 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170

Qy 361 TTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420

Db 1171 TTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1230

and Wilder, C.L.
TITLE Platelet-activating factor acetylhydrolase
JOURNAL Patent: US 6146625-A 30 14-NOV-2000;
FEATURES Location/Qualifiers
source 1..1335
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match		99.7%;	Score 512.4;	DB 6;	Length 1335;
Best Local Similarity		99.8%;	Pred. No. 3.8e-106;		
Matches	513;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
QY	1	GGACATTC	TTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA	60	
Db	811	GGACATTC	TTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA	870	
QY	61	TGTGGTATTGCCCTGGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT	120		
Db	871	TGTGGTATTGCCCTGGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT	930		
QY	121	CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATATCATAAAA	180		
Db	931	CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGCTAATATCATAAAA	990		
QY	181	ATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	240		
Db	991	ATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	1050		
QY	241	CACCAGAAATTTTGCTGACTTCACITTTTGCAACTGGCAAAATTAATTGGACACATGCTCAA	300		
Db	1051	CACCAGAAATTTTGCTGACTTCACITTTTGCAACTGGCAAAATTAATTGGACACATGCTCAA	1110		
QY	301	TAAAGGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA	360		
Db	1111	TAAAGGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA	1170		
QY	361	TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA	420		
Db	1171	TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA	1230		
QY	421	GGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAAACACACCAATCAACACATCATG	480		
Db	1231	GGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAAACACACCAATCAACACATCATG	1290		
QY	481	TTACAGAACTCTTCAGGAATAGAGAAATACAATT	514		
Db	1291	TTACAGAACTCTTCAGGAATAGAGAAATACAATT	1324		

Search completed: March 15, 2005, 20:51:06
Job time : 2455.96 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:16 ; Search time 332.798 Seconds
(without alignments)
9142.928 Million cell updates/sec

Title: US-09-922-067F-9_COPY_848_1361
Perfect score: 514
Sequence: 1 ggacattcttttggtagc.....aggaatagagaatacaatt 514

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	514	100.0	1361	2	AaQ81780 Human T-c
2	514	100.0	1361	3	Aaa52357 CDNA enco
3	514	100.0	1561	6	Ab167659 Oesophagu
4	513	99.8	1323	6	Aad36733 Human lip
5	512.4	99.7	1203	10	Adg73659 Human PAF
6	512.4	99.7	1335	2	Aat87072 Human pla
7	512.4	99.7	1335	3	Aaa10885 Synthetic
8	512.4	99.7	1335	3	Aaz24261 Human PAF
9	512.4	99.7	1335	4	Aad04165 Human pla
10	512.4	99.7	1335	4	Aac89078 Platelet-
11	512.4	99.7	1335	5	Aad24740 Human pla
12	512.4	99.7	1336	9	Ada19513 CDNA rela
13	512.4	99.7	1505	6	Abk92177 Prostate
14	512.4	99.7	1505	11	Adp64943 Human pho
15	512.4	99.7	1505	11	Adp65357 Human pla
16	512.4	99.7	1505	12	Adh43822 Human pla
17	512.4	99.7	1505	12	Adj74586 Human pla
18	512.4	99.7	1505	12	Adp12846 Reference
19	512.4	99.7	1505	13	Adr25259 Breast ca
20	512.4	99.7	1505	13	Adr14276 Human NF-

21	512.4	99.7	1505	13	ADP54610	Adp54610 Human PRO
22	512.4	99.7	1505	13	ADP23966	Adp23966 PRO polyP
23	512.4	99.7	1520	2	AAQ87947	Aaq87947 Human pla
24	512.4	99.7	1520	2	AAT80564	Aat80564 Human pla
25	512.4	99.7	1520	2	AAT63701	Aat63701 CDNA enco
26	512.4	99.7	1520	2	AAT87048	Aat87048 Human pla
27	512.4	99.7	1520	2	AAT96127	Aat96127 Human pla
28	512.4	99.7	1520	2	AAx08463	Aax08463 Human pla
29	512.4	99.7	1520	2	AAV08534	Aav08534 Human PAF
30	512.4	99.7	1520	3	AAA10861	Aaa10861 Human pla
31	512.4	99.7	1520	3	AAZ24240	Aaz24240 Human PAF
32	512.4	99.7	1520	3	AAA59579	Aaa59579 cDNA enco
33	512.4	99.7	1520	4	AAO04143	Aad04143 Human pla
34	512.4	99.7	1520	4	AAC89057	Aac89057 Platelet-
35	512.4	99.7	1520	5	AAO24719	Aad24719 Human pla
36	512.4	99.7	1520	9	ADA19490	Ada19490 Human pla
37	511.4	99.5	1320	4	AAO04168	Aad04168 Mouse-Hum
38	511.4	99.5	1320	4	AAO04169	Aad04169 Mouse-Hum
39	511.4	99.5	1563	10	ADG73667	Adg73667 Human HCB
40	511.4	99.5	1917	10	ADG73669	Adg73669 Human GCB
41	511.4	99.5	1929	10	ADG73671	Adg73671 Human aCB
42	509.2	99.1	572	2	AAQ81781	Aaq81781 Humam lym
43	403.6	78.5	2167	9	ADA19505	Ada19505 Dog plasm
44	403.6	78.5	2191	2	AAQ87949	Aaq87949 Canine pl
45	403.6	78.5	2191	2	AAT80581	Aat80581 Canine pl

ALIGNMENTS

RESULT 1
AAQ81780
ID AAQ81780 standard; cDNA; 1361 BP.

XX AAQ81780;

XX 25-MAR-2003 (revised)

DT 18-AUG-1995 (first entry)

XX Human T-cell lymphoma lipoprotein-associated phospholipase-A2.

XX T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2; enzyme;

KW atherosclerosis; diagnosis; therapy; antiarteriosclerotic; ss.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 38..1357

FT /*tag= a

XX WO9500649-A1.

XX 05-JAN-1995.

XX 24-JUN-1994; 94WO-GB001374.

XX 25-JUN-1993; 93GB-00013144.

XX 11-JAN-1994; 94GB-00000413.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Macphee CH, Tew DG, Southan CD, Hickey DMB, Gloger IS;

PI Lawrence GMP, Rice SQJ;

XX WPI; 1995-052086/07.

XX P-PSDB; AAR64928.

XX Purified lipoprotein associated phospholipase A2 - used to develop prods. for diagnosis and therapy, partic. inhibitors for treatment of atherosclerosis.

XX Claim 8; Page 19; 29pp; English.

CC This sequence encodes an enzyme which may be used in a method of
CC screening compounds to identify those compounds which inhibit Lp-PLA2
CC which involves contacting isolated Lp-PLA2 with a test compound and
CC measuring the rate of turnover of an enzyme substrate as compared with
CC the rate of turnover in the absence of the test compound. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX

SQ Sequence 1361 BP; 417 A; 273 C; 278 G; 393 T; 0 U; 0 Other;

Query Match 100.0%; Score 514; DB 2; Length 1361;
Best Local Similarity 100.0%; Pred. No. 2.5e-129;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db |||||||
QY 848 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 907
Db |||||||
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGATGAAGTATATCCAGAATT 120
Db |||||||
QY 908 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGATGAAGTATATCCAGAATT 967
Db |||||||
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCATATCTCTGCTAATATCAATAA 180
Db |||||||
QY 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCATATCTCTGCTAATATCAATAA 1027
Db |||||||
QY 181 ATGAAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 240
Db |||||||
QY 1028 ATGAAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 1087
Db |||||||
QY 241 CACCAGAAATTTGCTGCTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 300
Db |||||||
QY 1088 CACCAGAAATTTGCTGCTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 1147
Db |||||||
QY 301 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAACCAAGCTTCATTAGCA 360
Db |||||||
QY 1148 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAACCAAGCTTCATTAGCA 1207
Db |||||||
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGCAGTGGGACTGCTTGGATTGAA 420
Db |||||||
QY 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGCAGTGGGACTGCTTGGATTGAA 1267
Db |||||||
QY 421 GGAGATGATGAGAATCTTATCCAGGACCAACATTAACAACCAATCAACACATCATG 480
Db |||||||
QY 1268 GGAGATGATGAGAATCTTATCCAGGACCAACATTAACAACCAATCAACACATCATG 1327
Db |||||||
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db |||||||
QY 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db |||||||

RESULT 2
AAA52357
ID AAA52357 standard; cDNA; 1361 BP.
XX
AC AAA52357;
XX
DT 18-SEP-2000 (first entry)
XX
DE cDNA encoding human low density lipoprotein-associated phospholipase A2.
XX
KW Human; low density lipoprotein associated phospholipase A2; LDL-PLA2;
KW plasma PAF acetyl hydroxylase; recombinant; purification;
KW short chain phospholipid; serine-dependant phospholipase; inflammation;
KW proinflammatory; anti inflammatory; drug screening; antibody; diagnosis;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 38..1360
FT /tag= a
FT /partial
FT /product= "Human LDL-PLA2"

FT /note= "No stop codon given in the specification"
XX
PN WO200024910-A1.
XX
PD 04-MAY-2000.
XX
PF 27-OCT-1999; 99WO-GB003551.
XX
PR 28-OCT-1998; 98GB-00023647.
PR 28-OCT-1998; 98GB-00023648.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Boyd H, Tew DG;
PI WPI; 2000-350749/30.
DR P-PSDB; AAB01942.
DR
XX
PT Recombinant low density lipoprotein associated phospholipase A2, used to
PT produce antibodies for diagnostics, is purified using a Blue Sepharose
PT and Q Sepharose column.
PS Claim 6d; Page 15-17; 28pp; English.
XX
CC The present sequence represents cDNA encoding human LDL-PLA2. The
CC invention relates to a method for purifying recombinant low density
CC lipoprotein-associated phospholipase A2 (LDL-PLA2). The method comprises
CC applying a cell extract, supernatant or solution containing the
CC recombinantly expressed LDL-PLA2 to a zinc chelating column, applying the
CC eluate to a Blue Sepharose column, and applying that eluate to a Q
CC Sepharose column. The invention also provides a process which
CC additionally comprises the prior steps of constructing a vector
CC comprising a cDNA encoding a histidine tagged LDL-PLA2 or fragment
CC thereof, expressing the tagged protein in a host cell, isolating the
CC tagged protein from the harvest medium or cell lysate, purifying the
CC protein using a metal matrix affinity column (preferably a nickel
CC column), and removing the histidine tag by protease cleavage. LDL-PLA2,
CC also known as plasma PAF acetyl hydroxylase, is a serine-dependent
CC phospholipase which catalyses the hydrolysis of phospholipids with short
CC chain acyl groups at the sn-2 position. Its in vivo role is not known -
CC due to its ability to hydrolyse both phospholipids with short chain sn-2
CC substituents (which often arise from oxidative cleavage of longer chain
CC sn-2 substituents) and PAF, it may be either a pro-inflammatory enzyme or
CC an anti-inflammatory enzyme, depending on the precise in vivo role
CC adopted. LDL-PLA2 can be used in structural and mechanistic studies to
CC elucidate the activity of the enzyme in vivo. The enzyme may be used to
CC screen and identify compounds which modulate its activity, and to raise
CC antibodies for use in diagnostics
XX
SQ Sequence 1361 BP; 417 A; 273 C; 278 G; 393 T; 0 U; 0 Other;

Query Match 100.0%; Score 514; DB 3; Length 1361;
Best Local Similarity 100.0%; Pred. No. 2.5e-129;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db |||||||
QY 848 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 907
Db |||||||
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGATGAAGTATATCCAGAATT 120
Db |||||||
QY 908 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGATGAAGTATATCCAGAATT 967
Db |||||||
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCAATAA 180
Db |||||||
QY 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCAATAA 1027
Db |||||||
QY 181 ATGAAAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 240
Db |||||||
QY 1028 ATGAAAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 1087
Db |||||||
QY 241 CACCAGAAATTTGCTGCTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 300
Db |||||||

Db 1088 CACCAGAAATTTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAA 1147
Qy 301 TTTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1148 TTTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207
Qy 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1208 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1267
Qy 421 GGAGATGATGAGAATCTTTATTCAGGGACCAACATTAACACACCAATCAACACATCATG 480
Db 1268 GGAGATGATGAGAATCTTTATTCAGGGACCAACATTAACACACCAATCAACACATCATG 1327
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 3

ABL67659
ID ABL67659 standard; DNA; 1561 BP.
XX
AC ABL67659;
XX
DT 15-MAY-2002 (first entry)
XX
DE Oesophagus cancer related gene sequence SEQ ID NO:5996.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.

PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 5996; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 1561 BP; 447 A; 337 C; 352 G; 425 T; 0 U; 0 Other;
Query Match 100.0%; Score 514; DB 6; Length 1561;
Best Local Similarity 100.0%; Pred. No. 2.6e-129;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGACATTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 60
Db 1027 GGACATTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 1086
Qy 61 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1087 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1146
Qy 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATCATATAAA 180
Db 1147 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATCATATAAA 1206
Qy 181 ATGAAAAAATGCTACTCACCTGATATAAAGAAAGATGATTACAATCAGGGGTTGAGTC 240
Db 1207 ATGAAAAAATGCTACTCACCTGATATAAAGAAAGATGATTACAATCAGGGGTTGAGTC 1266
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1267 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1326
Qy 301 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCAATTAGCA 360
Db 1327 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCAATTAGCA 1386

PR 28-MAR-2002; 2002JP-00090847.
XX (SEGK) SEIKAGAKU KOGYO CO LTD.
PA
XX WPI; 2003-869686/81.
DR P-PSDB; ADG73660.
XX
PT Novel bioactive protein binding with collagen and having platelet
PT activating factor and acetyl hydrolase activity, useful for suppressing
PT local inflammation.
XX
XX Claim 7; SEQ ID NO 7; 53pp; Japanese.
PS
XX The invention relates to a novel bioactive protein binding with collagen
CC having platelet activating factor and acetyl hydrolase activity, and
CC comprising collagen coupling region. A protein of the invention has
CC antiinflammatory activity. A protein of the invention is useful for
CC suppressing local inflammation caused during skin transplantation. The
CC present sequence is used in the exemplification of the invention.
XX
SQ Sequence 1203 BP; 379 A; 231 C; 244 G; 349 T; 0 U; 0 Other;
Query Match 99.7%; Score 512.4; DB 10; Length 1203;
Best Local Similarity 99.8%; Pred. No. 6.5e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db 688 GGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 747
Qy 61 TGTGGTATTGCCCTGGATGGATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
Db 748 TGTGGTATTGCCCTGGATGGATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 807
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGCTAATATCATAAAA 180
Db 808 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGCTAATATCATAAAA 867
Qy 181 ATGAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 240
Db 868 ATGAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 927
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 300
Db 928 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 987
Qy 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db 988 TTAAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1047
Qy 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTGATTGAA 420
Db 1048 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTGATTGAA 1107
Qy 421 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 480
Db 1108 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 1167
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
Db 1168 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1201

RESULT 6
AAT87072
ID AAT87072 standard; cDNA; 1335 BP.

XX AAT87072;
XX
XX 25-MAR-2003 (revised)
DT 06-JAN-1998 (first entry)
XX
DE Human platelet-activating factor acetylhydrolase modified cDNA.

XX Platelet-activating factor acetylhydrolase; PAF-AH; human; inflammation;
KW asthma; pleurisy; necrotising enterocolitis;
KW adult respiratory distress syndrome; therapy; ss.
XX
OS Homo sapiens.
OS Mus musculus.
OS Synthetic.
OS Chimeric.
XX
PN US5656431-A.
XX 12-AUG-1997.
PD
XX
PF 07-JUN-1995; 95US-00483232.
XX
PR 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;
PI Eberhardt CD;
XX
DR WPI; 1997-414580/38.
DR P-PSDB; AAW26498.
XX
PT Detecting lesions in human platelet-activating factor acetylhydrolase
PT gene - by comparison with defined wild-type gene sequence.
XX
PS Example 8; Col 79-82; 53pp; English.
XX
CC This cDNA sequence codes for human platelet-activating factor
CC acetylhydrolase (PAF-AH) (AAW26498), a plasma protein that inactivates
CC PAF and oxidatively fragmented phospholipids such as products of the
CC arachidonic acid cascade that mediate inflammation. The codon usage of
CC the first 290 bp of the coding sequence was altered in an attempt to
CC boost expression levels of the human protein in transfected mammalian
CC cells. A synthetic 290 bp DNA fragment produced by PCR was ligated with
CC DNA encoding the remainder of the human PAF-AH molecule and inserted into
CC mammalian expression vector pRC/CMV. A murine 5' flanking sequence was
CC used adjacent to the human PAF-AH coding sequence. Use of this vector
CC increased expression of human PAF-AH from a few ng/ml to about 0.5 um/ml
CC in a transient COS cell transfection. (Updated on 25-MAR-2003 to correct
CC PF field.)
XX
SQ Sequence 1335 BP; 406 A; 277 C; 286 G; 366 T; 0 U; 0 Other;
Query Match 99.7%; Score 512.4; DB 2; Length 1335;
Best Local Similarity 99.8%; Pred. No. 6.7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db 811 GGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870
Qy 61 TGTGGTATTGCCCTGGATGGATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
Db 871 TGTGGTATTGCCCTGGATGGATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 930
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGCTAATATCATAAAA 180
Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGCTAATATCATAAAA 990
Qy 181 ATGAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 240
Db 991 ATGAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 1050
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 300
Db 1051 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 1110
Qy 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360

Db 1111 TAAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAGTGGGACTGCTTGATTGAA 420
Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAGTGGGACTGCTTGATTGAA 1230
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACACAAACCAATCAACATCATG 480
Db 1231 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACACAAACCAATCAACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 7
AAA10885
ID AAA10885 standard; cDNA; 1335 BP.
XX
AC AAA10885;
DT 14-JUL-2000 (first entry)
XX
DE Synthetic PAF-AH coding seugence used in PAF-AH construct.
KW Platelet-activating factor acetyl hydrolase; PAF-AH; PAF; phospholipid;
KW inflammatory response; pre-term labour; pharmaceutical composition;
KW regulate; asthma; anaphylaxis; shock; arthritis; Crohn's disease; ss;
KW pancreatitis; allergic inflammation; human immunodeficiency virus; HIV.
OS Synthetic.
XX
XX US6045794-A.
XX
XX 04-APR-2000.
XX
XX 09-JUN-1999; 99US-00328474.
XX
XX 06-OCT-1993; 93US-00133803.
XX
XX 06-OCT-1994; 94US-00318905.
XX
XX 07-JUN-1995; 95US-00483232.
XX
XX 12-AUG-1997; 97US-00910041.

PA (ICOS-) ICOS CORP.
XX
XX Cousins LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;
PI Eberhardt CD;
XX
XX WPI; 2000-282671/24.
XX
XX Treatment of mammals suffering from pre-term labor comprises
PT administering a pharmaceutical composition comprising platelet-activating
PT factor acetyl hydrolase enzyme.
XX
XX Example 8; Col 99-102; 67pp; English.
PS
XX
XX This sequence represents a recorded nucleotide sequence encoding platelet-
CC activating factor acetyl hydrolase (PAF-AH). PAF is a phospholipid and is
CC implicated in pathological inflammatory responses (e.g. asthma,
CC anaphylaxis, septic shock and arthritis). PAF-AH is released by
CC hepatocytes, and macrophages and inactivates PAF. PAF-AH also inactivates
CC oxidatively fragmented phospholipids that mediate inflammation. The human
CC PAF-AH nucleotide and protein sequences (see AAA10861 and AAY88301) is
CC specifically claimed for use in a method to treat a mammal suffering from
CC pre-term labour. PAF-AH is included in a pharmaceutical composition which
CC can be administered to a mammal suffering from pre-term labour. The
CC invention relates to purified and isolated polynucleotide sequences
CC encoding human PAF-AH and materials and methods for the recombinant
CC production of PAF-AH products which are expected to be useful in
CC regulating inflammatory events. The administration of PAF-AH to animals
CC may be used for ameliorating pathological inflammatory conditions such as
CC asthma, anaphylaxis, shock, arthritis, Crohn's disease, pancreatitis,

CC allergic inflammation, and human immunodeficiency virus (HIV)
XX
SQ Sequence 1335 BP; 406 A; 277 C; 286 G; 366 T; 0 U; 0 Other;
Query Match 99.7%; Score 512.4; DB 3; Length 1335;
Best Local Similarity 99.8%; Pred. No. 6.7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 811 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 870
QY 61 TGTGGTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 871 TGTGGTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 930
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTCTGCTAATATCATATAAA 180
Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTCTGCTAATATCATATAAA 990
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 991 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1050
QY 241 CACCAGAAATTTTGTGCTGACTTCACCTTTTGCACACTGGCAAAATAATTGGACACATGCTCAA 300
Db 1051 CACCAGAAATTTTGTGCTGACTTCACCTTTTGCACACTGGCAAAATAATTGGACACATGCTCAA 1110
QY 301 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTTCATCAGTGGGACTGCTTGATTGAA 420
Db 1171 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTTCATCAGTGGGACTGCTTGATTGAA 1230
QY 421 GGAGATGATGAGAATCTTATCCAGGGACCAACATTAACACAAACCAATCAACATCATG 480
Db 1231 GGAGATGATGAGAATCTTATCCAGGGACCAACATTAACACAAACCAATCAACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 8
AAZ24261
ID AAZ24261 standard; cDNA; 1335 BP.
XX
AC AAZ24261;
XX
DT 08-FEB-2000 (first entry)
XX
DE Human PAF-AH cDNA fragment.
XX
KW Platelet activating factor acetylhydrolase; PAF-AH; human; treatment;
KW antiinflammatory; antiasthmatic; antiallergic; antiarthritic; asthma;
KW antiischemic; inflammatory disorder; anaphylaxis; ulcerative colitis;
KW antigen-induced arthritis; ischemia; septicemia; allergy; ss.
OS Homo sapiens.
XX
XX US5977308-A.
PN
XX
PD 02-NOV-1999.
XX
XX 12-AUG-1997; 97US-00910041.
PF
XX 06-OCT-1993; 93US-00133803.
PR
XX 06-OCT-1994; 94US-00318905.
PR
XX 07-JUN-1995; 95US-00483232.
XX
PA (ICOS-) ICOS CORP.

XX Cousins LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;
PI Eberhardt CD;
PI
XX WPI; 2000-021956/02.
XX Truncated and substituted versions of human platelet activating factor
PT acetylhydrolase, for treating or preventing inflammatory diseases such as
PT asthma.
XX
XX
PS Example 8; Col 95-98; 65pp; English.
XX
XX This invention describes novel truncated and variant forms (I) of human
CC PAF-AH (platelet activating factor acetylhydrolase) which have
CC antiinflammatory, antiasthmatic, antiallergic, antiarthritic and
CC antiischemic activity. (I) are used to treat a wide variety of
CC inflammatory disorders, e.g. asthma, anaphylaxis, antigen-induced
CC arthritis, ulcerative colitis, ischemia, septicemia, allergy, etc.
CC Recombinant (I), produced in prokaryotic cells, are less heterogeneous at
CC the termini than the full-length protein. Some of the truncated versions
CC also have greater activity than the wild-type enzyme. This sequence
CC represents a human PAF-AH DNA fragment which is used in the construction
CC of plasmid pRC/HPH.4
XX
SQ Sequence 1335 BP; 406 A; 277 C; 286 G; 366 T; 0 U; 0 Other;

Query Match 99.7%; Score 512.4; DB 3; Length 1335;
Best Local Similarity 99.8%; Pred. No. 6.7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db |||||||
811 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870
QY 61 TGTGGTATTGGCCTGGATGCATGGATGTTTCCACTGGGTGAAGATATATCCAGAATT 120
Db |||||||
871 TGTGGTATTGGCCTGGATGCATGGATGTTTCCACTGGGTGAAGATATATCCAGAATT 930
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGTAATATCATAAAA 180
Db |||||||
931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGTAATATCATAAAA 990
QY 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTCAGTC 240
Db |||||||
991 ATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTCAGTC 1050
QY 241 CACCAGAAATTTGCTGACTTCACCTTTTGCACTGGCAAAATAATTGGACACATGCTCAA 300
Db |||||||
1051 CACCAGAAATTTGCTGACTTCACCTTTTGCACTGGCAAAATAATTGGACACATGCTCAA 1110
QY 301 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db |||||||
1111 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGTTGATTGAA 420
Db |||||||
1171 TTCTTACAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGTTGATTGAA 1230
QY 421 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 480
Db |||||||
1231 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
Db |||||||
1291 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1324

RESULT 9
AAD04165
ID AAD04165 standard; DNA; 1335 BP.
XX
AC AAD04165;
XX

DT 02-JUL-2001 (first entry)
XX Human plasma platelet-activating factor (PAF)-AH recorded gene.
DE
XX
KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
KW antiinflammatory; septicemia; inflammation; haemostasis; parturition;
KW asthma; anaphylaxis; septic shock; antibacterial; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6203790-B1.
XX
PD 20-MAR-2001.
XX
PF 23-MAY-2000; 2000US-00577758.
XX
PR 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
PR 07-JUN-1995; 95US-00480658.
PR 22-JAN-1998; 98US-00010715.
XX
PA (ICOS-) ICOS CORP.
XX
PI Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
PI Wilder CL;
XX
DR WPI; 2001-280610/29.
XX
XX Treating a mammal susceptible to or suffering from septicemia comprises
PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
PT supplement endogenous PAF-AH activity and to inactivate pathological
PT amounts of PAF.
XX
PS Example 8; Col 79-80; 54pp; English.
XX
XX The present DNA sequence is human plasma platelet-activating factor
CC acetylhydrolase (PAF-AH) recorded gene. First 290 bases of the PAF-AH
CC coding sequence was recoded, in which most of the codons have been
CC substituted with a codon of different sequence but encoding the same
CC amino acid was constructed. This recoded gene is successful in boosting
CC the expression levels of human PAF-AH from a few nanograms/ml to about
CC 0.5 microgram/ml in a transient COS cell transfection system. The
CC invention relates to human plasma platelet-activating factor
CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
CC invention also relates to method of treating a mammal susceptible to or
CC suffering from septicemia. PAF functions in normal physiological
CC processes such as inflammation, haemostasis and parturition. PAF-AH
CC specific antibodies are used in the diagnostic methods to detect abnormal
CC levels of PAF-AH in serum and also for treating the pathological
CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
CC shock and arthritis. PAF-AH antibody is also useful for screening a
CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
CC replacement of nucleotide G to T at position 996 within exon 9 resulting
CC in replacement of amino acid Val to Phe at position 279. Thus the
CC deficiency of PAF-AH activity is due to the genetic lesion in human
CC plasma PAF-AH gene
XX
SQ Sequence 1335 BP; 406 A; 277 C; 286 G; 366 T; 0 U; 0 Other;

Query Match 99.7%; Score 512.4; DB 4; Length 1335;
Best Local Similarity 99.8%; Pred. No. 6.7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db |||||||
811 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGAAGATATATCCAGAATT 120
Db |||||||
871 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGAAGATATATCCAGAATT 930
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGTAATATCATAAAA 180

PR 23-MAY-2000; 2000US-00577758.
XX (ICOS-) ICOS CORP.
XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
PI Wilder CL;
XX WPI; 2001-595771/67.
XX Composition for treating e.g. pleurisy, asthma, rhinitis, necrotizing
PT enterocolitis or acute respiratory distress syndrome, comprises platelet
PT activating factor acetyl hydrolase.
XX
XX Example 8; Page 43-44; 55pp; English.
XX The patent discloses human plasma platelet activating factor acetyl
CC hydrolase (PAF-AH) enzyme and its corresponding polynucleotides. The
CC invention also relates to compositions comprising PAF-AH which are useful
CC for regulating pathological inflammatory events. They are also useful for
CC treating PAF-mediated pathological conditions such as pleurisy, asthma,
CC rhinitis, necrotizing enterocolitis or acute respiratory distress
CC syndrome. The present sequence is human plasma PAF-AH genomic DNA
XX
SQ Sequence 1335 BP; 406 A; 277 C; 286 G; 366 T; 0 U; 0 Other;

Query Match 99.7%; Score 512.4; DB 5; Length 1335;
Best Local Similarity 99.8%; Pred. No. 6.7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
811 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870
Qy 61 TGTGGTATTCGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
871 TGTGGTATTCGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 930
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATAAAA 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATAAAA 990
Qy 181 ATGAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
991 ATGAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1050
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGGCAAAATTAATTGGACATGCTCAAA 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1051 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGGCAAAATTAATTGGACATGCTCAAA 1110
Qy 301 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1111 TTAAAGGGAGACATAGATTCAAAATGTAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
Qy 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1171 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1230
Qy 421 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAAACACAAATCAACACATCATG 480
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1231 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAAACACAAATCAACACATCATG 1290
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 12
ADA19513
ID ADA19513 standard; cDNA; 1336 BP.
XX
AC ADA19513;
XX 20-NOV-2003 (first entry)
DT

XX cDNA related to human plasma platelet-activating factor acetylhydrolase.
XX
XX pharmaceutical composition; human;
KW plasma platelet-activating factor acetylhydrolase; plasma PAF-AH; enzyme;
KW antiasthmatic; antiallergic; antiinflammatory;
KW platelet activating factor; PAF; inflammation;
KW PAF-mediated pathological condition; endogenous PAF-AH activity;
KW pleurisy; asthma; rhinitis; necrotizing enterocolitis;
KW acute respiratory distress syndrome; gene; ss.
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1..1335
FT /*tag= a
FT /product= "Human plasma PAF-AH"
FT /transl_except= (145..148, aa:Ala)
FT /transl_except= (169..184, aa:PRGNG)
XX
PN US2003072747-A1.
XX
PD 17-APR-2003.
XX
PF 13-OCT-2001; 2001US-00003978.
XX
PR 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
PR 07-JUN-1995; 95US-00480658.
PR 22-JAN-1998; 98US-00010715.
PR 23-MAY-2000; 2000US-00577758.
PR 04-DEC-2000; 2000US-00729402.
XX (ICOS-) ICOS CORP.
XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
PI Wilder CL;
XX WPI; 2003-576471/54.
DR P-PSDB; ADA19491.
XX
XX Pharmaceutical composition for treating a mammal suffering from platelet
PT activating factor-mediated pathological condition e.g. asthma, comprises
PT human plasma platelet-activating factor acetylhydrolase enzyme.
XX
PS Example 8; Page 43-44; 55pp; English.
XX
CC This invention relates to a novel pharmaceutical composition comprising
CC human plasma platelet-activating factor acetylhydrolase (PAF-AH) enzyme
CC and a pharmaceutically acceptable diluent, adjuvant or carrier. The
CC compound of the invention may have antiasthmatic, antiallergic or
CC antiinflammatory activities by blocking platelet activating factor (PAF)
CC induced inflammation. The compound of the invention may therefore be
CC useful for the treatment of a mammal susceptible to or suffering from a
CC PAF-mediated pathological condition, by administering the compound to the
CC mammal in an amount sufficient to supplement endogenous PAF-AH activity
CC and to inactivate pathological amounts of PAF in the mammal. The PAF-
CC mediated pathological conditions include pleurisy, asthma, rhinitis,
CC necrotizing enterocolitis and acute respiratory distress syndrome. The
CC present sequence is that of a cDNA, encoding the human plasma platelet-
CC activating factor acetylhydrolase (PAF-AH) enzyme of the invention, in
CC which most of the codons have been substituted with a codon encoding the
CC same amino acid.
XX
SQ Sequence 1336 BP; 406 A; 278 C; 286 G; 366 T; 0 U; 0 Other;

Query Match 99.7%; Score 512.4; DB 9; Length 1336;
Best Local Similarity 99.8%; Pred. No. 6.7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
|||

Db 812 GGACATCTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 871
QY 61 TGTGGTATTGCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 872 TGTGGTATTGCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 931
QY 121 CCTCAGCCCTCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 180
Db 932 CCTCAGCCCTCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 991
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 992 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1051
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1052 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1111
QY 301 TTAAGGGGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db 1112 TTAAGGGGACATAGATTCAAATGTAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1171
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1172 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1231
QY 421 GGAGATGATGAGAATCTTTATTCAGGGACCAACATTAACAACAACCAATCAACACATCATG 480
Db 1232 GGAGATGATGAGAATCTTTATTCAGGGACCAACATTAACAACAACCAATCAACACATCATG 1291
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1292 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1325

RESULT 13
ABK92177
ID ABK92177 standard; DNA; 1505 BP.
XX
AC ABK92177;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #63.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR WPI; 2002-471335/50.
DR P-PSDB; ABG61862.

XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 347; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;
Query Match 99.7%; Score 512.4; DB 6; Length 1505;
Best Local Similarity 99.8%; Pred. No. 7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACATCTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 972 GGACATCTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 1031
QY 61 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1032 TGTGGTATTGCCCTGGATGCGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091
QY 121 CCTCAGCCCTCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 180
Db 1092 CCTCAGCCCTCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 1151
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1152 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1212 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1271
QY 301 TTAAGGGGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db 1272 TTAAGGGGACATAGATTCAAATGTAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1331
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1332 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1391
QY 421 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACAACAACCAATCAACACATCATG 480
Db 1392 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACAACAACCAATCAACACATCATG 1451
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 14
ADP64943
ID ADP64943 standard; DNA; 1505 BP.
XX
AC ADP64943;

XX The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This polynucleotide
CC represents a DNA sequence relating to the genes used in the analysis and
CC treatment of autoimmune diseases or arthritides. Note: This sequence is
CC not shown in the specification. It has been supplied in an electronic
CC format from WIPO.

XX
SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.7%; Score 512.4; DB 11; Length 1505;
Best Local Similarity 99.8%; Pred. No. 7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db |||||||
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db |||||||
QY 1032 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091
Db |||||||
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATATAAA 180
Db |||||||
QY 1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATATAAA 1151
Db |||||||
QY 181 ATGAAAAAATGCTACTCCTGATGATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db |||||||
QY 1152 ATGAAAAAATGCTACTCCTGATGATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211
Db |||||||
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db |||||||
QY 1212 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1271
Db |||||||
QY 301 TTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db |||||||
QY 1272 TTAAGGGGAGACATAGATTCAAATGTAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1331
Db |||||||
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAAGTGGGACTGCTTGATTGAA 420
Db |||||||
QY 1332 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAAGTGGGACTGCTTGATTGAA 1391
Db |||||||
QY 421 GGAGATGATGAGAATCTTATTTCCAGGGACCAACATTAAACAACCAATCAACACATCATG 480
Db |||||||
QY 1392 GGAGATGATGAGAATCTTATTTCCAGGGACCAACATTAAACAACCAATCAACACATCATG 1451
Db |||||||
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db |||||||
QY 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485
Db |||||||

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:21 ; Search time 103.622 Seconds
(without alignments)
8116.452 Million cell updates/sec

Title: US-09-922-067F-9_COPY_848_1361
Perfect score: 514
Sequence: 1 ggacattttttgtggagc.....aggaatagagaatacaatt 514

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514	100.0	1361	2	US-08-557-892-9 Sequence 9, Appli
2	514	100.0	1361	2	US-08-387-858A-9 Sequence 9, Appli
3	514	100.0	1361	3	US-09-294-384B-9 Sequence 9, Appli
4	514	100.0	1361	3	US-08-717-079-9 Sequence 9, Appli
5	512.4	99.7	1335	1	US-08-483-232-30 Sequence 30, Appl
6	512.4	99.7	1335	2	US-08-485-938A-30 Sequence 30, Appl
7	512.4	99.7	1335	2	US-08-910-041-30 Sequence 30, Appl
8	512.4	99.7	1335	3	US-09-328-474-30 Sequence 30, Appl
9	512.4	99.7	1335	3	US-09-100-546-30 Sequence 30, Appl
10	512.4	99.7	1335	3	US-09-010-715-30 Sequence 30, Appl
11	512.4	99.7	1335	3	US-09-577-758-30 Sequence 30, Appl
12	512.4	99.7	1520	1	US-08-470-187-7 Sequence 7, Appli
13	512.4	99.7	1520	1	US-08-318-905-7 Sequence 7, Appli
14	512.4	99.7	1520	1	US-08-483-232-7 Sequence 7, Appli
15	512.4	99.7	1520	1	US-08-483-140-7 Sequence 7, Appli
16	512.4	99.7	1520	2	US-08-485-938A-7 Sequence 7, Appli
17	512.4	99.7	1520	2	US-08-910-041-7 Sequence 7, Appli
18	512.4	99.7	1520	3	US-09-328-474-7 Sequence 7, Appli
19	512.4	99.7	1520	3	US-09-100-546-7 Sequence 7, Appli
20	512.4	99.7	1520	3	US-09-010-715-7 Sequence 7, Appli
21	512.4	99.7	1520	3	US-09-577-758-7 Sequence 7, Appli
22	509.2	99.1	572	2	US-08-557-892-8 Sequence 8, Appli
23	509.2	99.1	572	2	US-08-387-858A-8 Sequence 8, Appli
24	509.2	99.1	572	3	US-09-294-384B-8 Sequence 8, Appli
25	509.2	99.1	572	3	US-08-717-079-8 Sequence 8, Appli
26	403.6	78.5	2191	1	US-08-318-905-22 Sequence 22, Appl
27	403.6	78.5	2191	1	US-08-483-232-22 Sequence 22, Appl

28	403.6	78.5	2191	1	US-08-483-140-22 Sequence 22, Appl
29	403.6	78.5	2191	2	US-08-485-938A-22 Sequence 22, Appl
30	403.6	78.5	2191	2	US-08-910-041-22 Sequence 22, Appl
31	403.6	78.5	2191	3	US-09-328-474-22 Sequence 22, Appl
32	403.6	78.5	2191	3	US-09-100-546-22 Sequence 22, Appl
33	403.6	78.5	2191	3	US-09-010-715-22 Sequence 22, Appl
34	403.6	78.5	2191	3	US-09-577-758-22 Sequence 22, Appl
35	402	78.2	1533	1	US-08-483-232-23 Sequence 23, Appl
36	402	78.2	1533	2	US-08-485-938A-23 Sequence 23, Appl
37	402	78.2	1533	2	US-08-910-041-23 Sequence 23, Appl
38	402	78.2	1533	3	US-09-328-474-23 Sequence 23, Appl
39	402	78.2	1533	3	US-09-100-546-23 Sequence 23, Appl
40	402	78.2	1533	3	US-09-010-715-23 Sequence 23, Appl
41	402	78.2	1533	3	US-09-577-758-23 Sequence 23, Appl
C 42	390.2	75.9	420	2	US-08-557-892-5 Sequence 5, Appli
C 43	390.2	75.9	420	2	US-08-387-858A-5 Sequence 5, Appli
C 44	390.2	75.9	420	3	US-09-294-384B-5 Sequence 5, Appli
C 45	390.2	75.9	420	3	US-08-717-079-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-557-892-9
; Sequence 9, Application US/08557892
; Patent No. 5968818
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,892
; FILING DATE: 14 No. 5968818ember 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,858
; FILING DATE: 14 No. 5968818ember 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
US-08-557-892-9

Query Match 100.0%; Score 514; DB 2; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.1e-143;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAGATCAGAGATTCAGA 60
Db 848 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAGATCAGAGATTCAGA 907

QY 61 TGTGGTATTGCCCTGGATGCAATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 908 TGTGGTATTGCCCTGGATGCAATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATAAAA 180
Db 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATAAAA 1027

QY 181 ATGAAAAATGCTACTCCTGATATAAGAAAGATGATTAATCAATCAGGGTTTCAGTC 240
Db 1028 ATGAAAAATGCTACTCCTGATATAAGAAAGATGATTAATCAATCAGGGTTTCAGTC 1087

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 300
Db 1088 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 1147

QY 301 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1148 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207

QY 361 TTCTTACAAAAGCATTTAGACTTTCATAAAGATTTTGTAGTGGAGTGGCTTGAATTGAA 420
Db 1208 TTCTTACAAAAGCATTTAGACTTTCATAAAGATTTTGTAGTGGAGTGGCTTGAATTGAA 1267

QY 421 GGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACAACCAATCAACACATCATG 480
Db 1268 GGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACAACCAATCAACACATCATG 1327

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 2
US-08-387-858A-9
Sequence 9, Application US/08387858A
Patent No. 5981252
GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
APPLICANT: Tew, David Graham
APPLICANT: Southan, Christopher Donald
APPLICANT: Hickey, Dierdre Mary Bernadette
APPLICANT: Glover, Israel Simon
APPLICANT: Lawrence, Geoffrey Mark Prouse
APPLICANT: Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,858A
FILING DATE: 24 February 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
US-08-387-858A-9

Query Match 100.0%; Score 514; DB 2; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.1e-143;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAGATCAGAGATTCAGA 60
Db 848 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAGATCAGAGATTCAGA 907

QY 61 TGTGGTATTGCCCTGGATGCAATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 908 TGTGGTATTGCCCTGGATGCAATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATAAAA 180
Db 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATAAAA 1027

QY 181 ATGAAAAATGCTACTCCTGATATAAGAAAGATGATTAATCAATCAGGGTTTCAGTC 240
Db 1028 ATGAAAAATGCTACTCCTGATATAAGAAAGATGATTAATCAATCAGGGTTTCAGTC 1087

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 300
Db 1088 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 1147

QY 301 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1148 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207

QY 361 TTCTTACAAAAGCATTTAGACTTTCATAAAGATTTTGTAGTGGAGTGGCTTGAATTGAA 420
Db 1208 TTCTTACAAAAGCATTTAGACTTTCATAAAGATTTTGTAGTGGAGTGGCTTGAATTGAA 1267

QY 421 GGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACAACCAATCAACACATCATG 480
Db 1268 GGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACAACCAATCAACACATCATG 1327

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 3
US-09-294-384B-9
Sequence 9, Application US/09294384B
Patent No. 6177257

GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,384B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,858
; FILING DATE: 24 February 1995
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 38..1360
; US-09-294-384B-9

Query Match 100.0%; Score 514; DB 3; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.1e-143;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATCTTTTGGTGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAGATTGAGA 60
Db 848 GGACATCTTTTGGTGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAGATTGAGA 907

Qy 61 TGTGGTATTGGCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
Db 908 TGTGGTATTGGCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 967

Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
Db 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 1027

Qy 181 ATGAAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1028 ATGAAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087

Qy 241 CACCAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1088 CACCAGAAATTTTGTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1147

Qy 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1148 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207

Qy 361 TTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGTGATGAGTGGGACTGCTTATTGAA 420
Db 1208 TTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGTGATGAGTGGGACTGCTTATTGAA 1267

Qy 421 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAAACAAACCAATCAACACATCATG 480
Db 1268 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAAACAAACCAATCAACACATCATG 1327

Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 4
US-08-717-079-9
; Sequence 9, Application US/08717079
; Patent No. 6369045
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,079
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,858
; FILING DATE: 24 February 1995
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
US-08-717-079-9

Query Match 100.0%; Score 514; DB 3; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.1e-143;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTACTGAAGATCAGAGATTCAGA 60
Db 848 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTACTGAAGATCAGAGATTCAGA 907

QY 61 TGTGGTATTCGCCCTGGATGGATGTTTCCACTGGGATGAAGTATATCCAGAATT 120
Db 908 TGTGGTATTCGCCCTGGATGGATGTTTCCACTGGGATGAAGTATATCCAGAATT 967

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCAATAA 180
Db 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCAATAA 1027

QY 181 ATGAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1028 ATGAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1088 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAAA 1147

QY 301 TTAAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1207
Db 1148 TTAAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1207

QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1267

QY 421 GGAGATGATGAGAAATCTTATCCAGGACCAACATTAACAACCAATCAACACATCATG 480
Db 1268 GGAGATGATGAGAAATCTTATCCAGGACCAACATTAACAACCAATCAACACATCATG 1327

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 5
US-08-483-232-30
Sequence 30, Application US/08483232
Patent No. 5656431

GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,232
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5656431and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32689
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-483-232-30

Query Match 99.7%; Score 512.4; DB 1; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db 811 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870

QY 61 TGTGGTATTCGCCCTGGATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
Db 871 TGTGGTATTCGCCCTGGATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 930

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCAATAA 180
Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCAATAA 990

QY 181 ATGAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 991 ATGAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1050

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1051 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1110

QY 301 TTAAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1170
Db 1111 TTAAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1170

QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1230

QY 421 GGAGATGATGAGAAATCTTATCCAGGGACCAACATTAACAACCAATCAACACATCATG 480
Db 1231 GGAGATGATGAGAAATCTTATCCAGGGACCAACATTAACAACCAATCAACACATCATG 1290

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 6
US-08-485-938A-30
Sequence 30, Application US/08485938A
Patent No. 5847088
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.

APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5847088and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32792
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-485-938A-30

Query Match 99.7%; Score 512.4; DB 2; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACATCTTTGGTGGAGCAACGGTTATTAGACTCTTAGTGAAGATCAGAGATTGCA 60
DB 811 GGACATCTTTGGTGGAGCAACGGTTATTAGACTCTTAGTGAAGATCAGAGATTGCA 870
QY 61 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
DB 871 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 930
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTGCTAATATCATAAAA 180
DB 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTGCTAATATCATAAAA 990
QY 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 240
DB 991 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 1050
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCACTGGCAAAAATAATTGGACACATGCTCAA 300
DB 1051 CACCAGAAATTTGCTGACTTCACTTTTGCACTGGCAAAAATAATTGGACACATGCTCAA 1110
QY 301 TTAAGGGGAGACATAGATTCAATTCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360

Db 1111 TTAAGGGGAGACATAGATTCAATGTAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1171 TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1230
QY 421 GGAGATGATGAGAAATCTTATCCAGGGACCAACATTAAACACAACCAATCAACACATCATG 480
Db 1231 GGAGATGATGAGAAATCTTATCCAGGGACCAACATTAAACACAACCAATCAACACATCATG 1290
QY 481 TTACAGAACTCTTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1324

RESULT 7
US-08-910-041-30
; Sequence 30, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Coubens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-910-041-30

Query Match 99.7%; Score 512.4; DB 2; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;

	Matches	513;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	GGACATTTCTTTTGGTGGAGCAACGGTTATT	CAGACTCTTTAGTGAAGATCAGAGATT	CAGA	60					
DB	811	GGACATTTCTTTTGGTGGAGCAACGGTTATT	CAGACTCTTTAGTGAAGATCAGAGATT	CAGA	870					
QY	61	TGTGGTATTGCCCTGGATGCATGGATGTTTT	CCACTGGGTGATGAAGTATATTTCCAGAATT	120						
DB	871	TGTGGTATTGCCCTGGATGCATGGATGTTTT	CCACTGGGTGATGAAGTATATTTCCAGAATT	930						
QY	121	CCTCAGCCCCCTCTTTTTTATCAAACTCTGA	ATATTTCCAAATCCTGCTAATATCATATAAA	180						
DB	931	CCTCAGCCCCCTCTTTTTTATCAAACTCTGA	ATATTTCCAAATCCTGCTAATATCATATAAA	990						
QY	181	ATGAAAAAATGTCTACTCACCTGATAAAGA	AAAAAGATGATTACAATCAGGGGTTTCAGTC	240						
DB	991	ATGAAAAAATGTCTACTCACCTGATAAAGA	AAAAAGATGATTACAATCAGGGGTTTCAGTC	1050						
QY	241	CACCAGAAATTTGCTGACTTCACTTTTGCA	ACTGGCAAAATAATTGGACACATGCTCAA	300						
DB	1051	CACCAGAAATTTGCTGACTTCACTTTTGCA	ACTGGCAAAATAATTGGACACATGCTCAA	1110						
QY	301	TTAAAGGGGACATAGATTCAAATGCAGCT	TATTGATCTTTAGCAACAAGCTTCATTAGCA	360						
DB	1111	TTAAAGGGGACATAGATTCAAATGCAGCT	TATTGATCTTTAGCAACAAGCTTCATTAGCA	1170						
QY	361	TTCTTACAAAAGCATTTTAGCACTTCATA	AAAGATTTTGATCAGTGGGACTGCTTTGATTGAA	420						
DB	1171	TTCTTACAAAAGCATTTTAGCACTTCATA	AAAGATTTTGATCAGTGGGACTGCTTTGATTGAA	1230						
QY	421	GGAGATGATGAGAATCTTTATTCAGGGAC	CAACATTAACAACAACCAATCAACACATCATG	480						
DB	1231	GGAGATGATGAGAATCTTTATTCAGGGAC	CAACATTAACAACAACCAATCAACACATCATG	1290						
QY	481	TTACAGAACTCTTCCAGGAATAGAGAAAT	TACAATT	514						
DB	1291	TTACAGAACTCTTCCAGGAATAGAGAAAT	TACAATT	1324						

; APPLICATION NUMBER: US 08/318,905
 ; FILING DATE: 06-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rin-Laures, Li-Hsien
 ; REGISTRATION NUMBER: 33,547
 ; REFERENCE/DOCKET NUMBER: 27866/34026
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3658
 ; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1335 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; US-09-328-474-30

Query Match	99.7%;	Score 512.4;	DB 3;	Length 1335;	
Best Local Similarity	99.8%;	Pred. No. 3.2e-143;			
Matches 513;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	GGACATCTCTTTGGTGGAGCAACGGTTATT	CAGACTCTTAGTGAAGATCAGAGATT	CAGA	60
DB	811	GGACATCTCTTTGGTGGAGCAACGGTTATT	CAGACTCTTAGTGAAGATCAGAGATT	CAGA	870
QY	61	TGTGGTATTGCCCTGGATGTCATGGATGTT	CCACTGGGTGATGAAGTATAT	CCAGAATT	120
DB	871	TGTGGTATTGCCCTGGATGTCATGGATGTT	CCACTGGGTGATGAAGTATAT	CCAGAATT	930
QY	121	CCTCAGCCCTCTTTTATCAACTCTGAATAT	TTCCAAATATCCTGCTAAATATCATATAA	A	180
DB	931	CCTCAGCCCTCTTTTATCAACTCTGAATAT	TTCCAAATATCCTGCTAAATATCATATAA	A	990
QY	181	ATGAAAAAATGCTACTCACCTGATAAAGAA	AGAAAGATGATTACAATCAGGGGTT	CAGTC	240
DB	991	ATGAAAAAATGCTACTCACCTGATAAAGAA	AGAAAGATGATTACAATCAGGGGTT	CAGTC	1050
QY	241	CACCAGAAATTTGCTGACTTCACCTTTTG	CAACTGGCAAAATAATTGGACACATGCT	CAAA	300
DB	1051	CACCAGAAATTTGCTGACTTCACCTTTTG	CAACTGGCAAAATAATTGGACACATGCT	CAAA	1110
QY	301	TTAAAGGGAGACATAGATTCAAATGCAGCT	ATTGATCTTAGCAACAAGCTTCATTAGCA		360
DB	1111	TTAAAGGGAGACATAGATTCAAATGCAGCT	ATTGATCTTAGCAACAAGCTTCATTAGCA		1170
QY	361	TTCTTACAAAAGCATTTAGGACTTCATAA	AGATTTTGATCAGTGGGACTGCTTGATT	TGAA	420
DB	1171	TTCTTACAAAAGCATTTAGGACTTCATAA	AGATTTTGATCAGTGGGACTGCTTGATT	TGAA	1230
QY	421	GGAGATGATGAGAATCTTATTTCCAGGAC	CCAACATTAAACAAATCAACACATCAT	ATG	480
DB	1231	GGAGATGATGAGAATCTTATTTCCAGGAC	CCAACATTAAACAAATCAACACATCAT	ATG	1290
QY	481	TTACAGAACTCTTCAGGAATAGAGAAAT	ACAATT		514
DB	1291	TTACAGAACTCTTCAGGAATAGAGAAAT	ACAATT		1324

APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6099836and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-09-100-546-30

Query Match 99.7%; Score 512.4; DB 3; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db |
811 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870

QY 61 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db |
871 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 930

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
Db |
931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 990

QY 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 240
Db |
991 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 1050

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCACTGGCAAAATAATTTGGACACATGCTCAAA 300
Db |
1051 CACCAGAAATTTGCTGACTTCACTTTTGCACTGGCAAAATAATTTGGACACATGCTCAAA 1110

QY 301 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db |
1111 TTAAGGGAGACATAGATTCAAAATGTAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170

QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db |
1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1230

QY 421 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAAACAACCAATCAACACATCATG 480
Db |
1231 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAAACAACCAATCAACACATCATG 1290

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db |
1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 10
US-09-010-715-30
; Sequence 30, Application US/09010715
; Patent No. 6146625
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6146625and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-09-010-715-30

Query Match 99.7%; Score 512.4; DB 3; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db |
811 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870

QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 120
Db 871 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 930
QY 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
Db 931 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 990
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 991 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1050
QY 241 CACCAGAAATTTGCTGACTTTCACCTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1051 CACCAGAAATTTGCTGACTTTCACCTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAAA 1110
QY 301 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAAGGGAGACATAGATTCAAAATGTAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAGTGGGACTGCTTGATTGAA 420
Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAGTGGGACTGCTTGATTGAA 1230
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACAACCAATCAACACATCATG 480
Db 1231 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACAACCAATCAACACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 11

US-09-577-758-30
; Sequence 30, Application US/09577758
; Patent No. 6203790
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,758
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/010,715
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6203790and, Greta E.
; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-577-758-30

Query Match 99.7%; Score 512.4; DB 3; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 811 GGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 870
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 120
Db 871 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 930
QY 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
Db 931 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 990
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 991 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1050
QY 241 CACCAGAAATTTGCTGACTTTCACCTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1051 CACCAGAAATTTGCTGACTTTCACCTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAAA 1110
QY 301 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAAGGGAGACATAGATTCAAAATGTAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAGTGGGACTGCTTGATTGAA 420
Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCAGTGGGACTGCTTGATTGAA 1230
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACAACCAATCAACACATCATG 480
Db 1231 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACAACCAATCAACACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 12

US-08-470-187-7
; Sequence 7, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,187
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532152and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31672
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
US-08-470-187-7

Query Match 99.7%; Score 512.4; DB 1; Length 1520;
Best Local Similarity 99.8%; Pred. No. 3.4e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0;

Qy	1	GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAAGATCAGAGATTCAGA	60
Db	972	GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAAGATCAGAGATTCAGA	1031
Qy	61	TGTGGTATTGGCCCTGGATGCATGGATGTTTTCCACTGGGTGATGAAGTATATTCAGAAATT	120
Db	1032	TGTGGTATTGGCCCTGGATGCATGGATGTTTTCCACTGGGTGATGAAGTATATTCAGAAATT	1091
Qy	121	CCTCAGCCCTCTTTTTTATCAAACTCTGAATATTTCCAATATCCTGCTAATATCATATAAA	180
Db	1092	CCTCAGCCCTCTTTTTTATCAAACTCTGAATATTTCCAATATCCTGCTAATATCATATAAA	1151
Qy	181	ATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAAGATGATTACAATCAGGGGTTTCAGTC	240
Db	1152	ATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAAGATGATTACAATCAGGGGTTTCAGTC	1211
Qy	241	CACCAGAAATTTTGCTGACTTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAA	300
Db	1212	CACCAGAAATTTTGCTGACTTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAA	1271
Qy	301	TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA	360
Db	1272	TTAAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTAGCAACAAGCTTCATTAGCA	1331
Qy	361	TTCTTTACAAAAGCATTTAGGACTTCATAAGATTTTGATCAGTGGGACTGCTTGATTGAA	420
Db	1332	TTCTTTACAAAAGCATTTAGGACTTCATAAGATTTTGATCAGTGGGACTGCTTGATTGAA	1391
Qy	421	GGAGATGATGAGAAATCTTATTCCAGGGA CCAACATTAAACAACCAATCAACACATCATG	480
Db	1392	GGAGATGATGAGAAATCTTATTCCAGGGA CCAACATTAAACAACCAATCAACACATCATG	1451
Qy	481	TTACAGAACTCTTTCAGGAATAGAGAAATACAAATT	514
Db	1452	TTACAGAACTCTTTCAGGAATAGAGAAATACAAATT	1485

RESULT 13
US-08-318-905-7
; Sequence 7, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
US-08-318-905-7

	Query Match	99.7%;	Score 512.4;	DB 1;	Length 1520;
	Best Local Similarity	99.8%;	Pred. NO. 3.4e-143;		
	Matches 513;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	GGACATTC	TTTTGGTGGAGCAACGGTTATT	CAGACTCTTTAGTGAAGATCAGAGATT	CAGA 60
DB	972	GGACATTC	TTTTGGTGGAGCAACGGTTATT	CAGACTCTTTAGTGAAGATCAGAGATT	CAGA 1031
QY	61	TGTGATTTGCCCTGGATGCATGGATGTTTCCAC	TGGTGATGAAGTATAT	TCCAGAATT	120
DB	1032	TGTGATTTGCCCTGGATGCATGGATGTTTCCAC	TGGTGATGAAGTATAT	TCCAGAATT	1091
QY	121	CCTCAGCCCCCTCTTTTTTATCAACTCTGAATATTTCCAATAT	CTCTGCTAATATCATATA	180	
DB	1092	CCTCAGCCCCCTCTTTTTTATCAACTCTGAATATTTCCAATAT	CTCTGCTAATATCATATA	1151	
QY	181	ATGAAAAAATGCTACTCACCTGTATAAAGAAAGATGATTACAAT	CAGGGTTTCAGTC	240	

Db 1152 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211
QY 241 CACCAGAAATTTTGCTGACTTCACTTTTGGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1212 CACCAGAAATTTTGCTGACTTCACTTTTGGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1271
QY 301 TTAAGGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1272 TTAAGGGGAGACATAGATTCAAAATGTAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1331
QY 361 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 420
Db 1332 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 1391
QY 421 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 480
Db 1392 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 1451
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 14

US-08-483-232-7
; Sequence 7, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
US-08-483-232-7

Query Match 99.7%; Score 512.4; DB 1; Length 1520;
Best Local Similarity 99.8%; Pred. No. 3.4e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 972 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 1031
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1032 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091
QY 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTCTGCTAATATCATATAA 180
Db 1092 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTCTGCTAATATCATATAA 1151
QY 181 ATGAAAAAATGCTACTACCTGTATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1152 ATGAAAAAATGCTACTACCTGTATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211
QY 241 CACCAGAAATTTTGCTGACTTCACTTTTGGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1212 CACCAGAAATTTTGCTGACTTCACTTTTGGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1271
QY 301 TTAAGGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1272 TTAAGGGGAGACATAGATTCAAAATGTAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1331
QY 361 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 420
Db 1332 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 1391
QY 421 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 480
Db 1392 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACCAATCAACACATCATG 1451
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 15

US-08-483-140-7
; Sequence 7, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
US-08-483-140-7

Query Match 99.7%; Score 512.4; DB 1; Length 1520;
Best Local Similarity 99.8%; Pred. No. 3.4e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GGACATTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA	60
Db	972	GGACATTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA	1031
QY	61	TGTGGTATTCGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAAAT	120
Db	1032	TGTGGTATTCGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAAAT	1091
QY	121	CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA	180
Db	1092	CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAAA	1151
QY	181	ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	240
Db	1152	ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	1211
QY	241	CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA	300
Db	1212	CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA	1271
QY	301	TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA	360
Db	1272	TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA	1331
QY	361	TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTTGATTGAA	420
Db	1332	TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTTGATTGAA	1391
QY	421	GGAGATGATGAGAAATCTTATTCAGGGGACCAACATTAACACAAATCAACACATCATG	480
Db	1392	GGAGATGATGAGAAATCTTATTCAGGGGACCAACATTAACACAAATCAACACATCATG	1451
QY	481	TTACAGAACTCTTCAGGAATAGAGAAATACAAAT	514
Db	1452	TTACAGAACTCTTCAGGAATAGAGAAATACAAAT	1485

Search completed: March 15, 2005, 16:15:18
Job time : 104.622 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 16:15:21 ; Search time 501.116 Seconds
(without alignments)
6106.287 Million cell updates/sec

Title: US-09-922-067F-9_COPY_848_1361
Perfect score: 514
Sequence: 1 ggacattcttttggaggc.....aggaatagagaatacaatt 514

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	514	100.0	1361	9	US-09-922-067-9
2	514	100.0	1361	15	US-10-173-233-9
3	514	100.0	1361	16	US-10-406-156-9
4	514	100.0	1561	9	US-09-962-832-110
5	513.2	99.8	1845	18	US-10-741-601-89
6	513.2	99.8	1964	18	US-10-741-601-90
7	513	99.8	1323	18	US-10-415-682B-1
8	512.4	99.7	1335	9	US-09-729-402-30
9	512.4	99.7	1335	14	US-10-003-978A-30
10	512.4	99.7	1505	17	US-10-172-118-1120
11	512.4	99.7	1505	17	US-10-342-887-1120

12	512.4	99.7	1505	18	US-10-755-889-277
13	512.4	99.7	1520	9	US-09-729-402-7
14	512.4	99.7	1520	14	US-10-003-978A-7
15	509.2	99.1	572	9	US-09-922-067-8
16	509.2	99.1	572	15	US-10-173-233-8
17	509.2	99.1	572	16	US-10-406-156-8
18	403.6	78.5	2191	9	US-09-729-402-22
19	403.6	78.5	2191	14	US-10-003-978A-22
20	402	78.2	1533	9	US-09-729-402-23
21	402	78.2	1533	14	US-10-003-978A-23
22	399	77.6	477	10	US-09-918-995-24863
23	390.2	75.9	420	9	US-09-922-067-5
24	390.2	75.9	420	15	US-10-173-233-5
25	390.2	75.9	420	16	US-10-406-156-5
26	307.6	59.8	517	9	US-09-729-402-25
27	307.6	59.8	517	14	US-10-003-978A-25
28	302.8	58.9	379	9	US-09-922-067-6
29	302.8	58.9	379	15	US-10-173-233-6
30	302.8	58.9	379	16	US-10-406-156-6
31	284.6	55.4	1494	9	US-09-729-402-21
32	284.6	55.4	1494	14	US-10-003-978A-21
33	238.6	46.4	385	9	US-09-962-832-58
34	238.6	46.4	385	9	US-09-880-107-1974
35	238.6	46.4	385	11	US-09-968-007A-185
36	234.4	45.6	441	10	US-09-918-995-13782
37	215.8	42.0	1876	9	US-09-729-402-24
38	215.8	42.0	1876	14	US-10-003-978A-24
39	200.6	39.0	201	18	US-10-741-601-2009
40	200.6	39.0	201	18	US-10-741-601-2013
41	200.6	39.0	201	18	US-10-741-601-2017
42	200.6	39.0	201	18	US-10-741-601-2022
43	199.4	38.8	279	9	US-09-922-067-7
44	199.4	38.8	279	15	US-10-173-233-7
45	199.4	38.8	279	16	US-10-406-156-7

ALIGNMENTS

RESULT 1

US-09-922-067-9
; Sequence 9, Application US/09922067
; Patent No. US2002017209A1

GENERAL INFORMATION:

APPLICANT: MacPhee, Colin Houston
Tew, David Graham
Southan, Christopher Donald
Hickey, Dierdre Mary Bernadette
Gloger, Israel Simon
Lawrence, Geoffrey Mark Prouse
Rice, Simon Quentyn John

TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
Thereof And Use Of The Same In Diagnosis And Therapy

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road

CITY: King of Prussia

STATE: PA

COUNTRY: USA

ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/922,067

FILING DATE: 03-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/193,130

FILING DATE: 1998-11-17

APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-922-067-9

Query Match 100.0%; Score 514; DB 9; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATCTTTTGGTGAGCAACGGTTATTAGTGAAGATCAGAGATTTCAGA 60
Db |||||||
QY 61 TGTGGTATGCCCTGGATGATGGATTTCCACTGGGTGATGAAGTATATCCAGAAAT 120
Db |||||||
QY 908 TGTGGTATGCCCTGGATGATGGATTTCCACTGGGTGATGAAGTATATCCAGAAAT 967
Db |||||||
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 180
Db |||||||
QY 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 1027
Db |||||||
QY 181 ATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db |||||||
QY 1028 ATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087
Db |||||||
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db |||||||
QY 1088 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1147
Db |||||||
QY 301 TTAAGGGAGACATAGATTCAAATGCAGTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db |||||||
QY 1148 TTAAGGGAGACATAGATTCAAATGCAGTATTGATCTTAGCAACAAGCTTCATTAGCA 1207
Db |||||||
QY 361 TTCTTACAAAAGCATTATAGGACTTCAATAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 420
Db |||||||
QY 1208 TTCTTACAAAAGCATTATAGGACTTCAATAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 1267
Db |||||||
QY 421 GGAGATGATGAGAAATCTTATTTCCAGGACCAACATTAACAACAACCAATCAACATCATG 480
Db |||||||
QY 1268 GGAGATGATGAGAAATCTTATTTCCAGGACCAACATTAACAACAACCAATCAACATCATG 1327
Db |||||||
QY 481 TTACAGAACTCTTTCAGGAATAGAGAAATACAATT 514
Db |||||||
QY 1328 TTACAGAACTCTTTCAGGAATAGAGAAATACAATT 1361
Db |||||||

RESULT 2
US-10-173-233-9
; Sequence 9, Application US/10173233
; Publication No. US20030148398A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham

Southan, Christopher Donald
Hickey, Dierdre Mary Bernadette
Gloger, Israel Simon
Lawrence, Geoffrey Mark Prouse
Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/173,233
FILING DATE: 14-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/569,899
FILING DATE: 12-May-2000
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-173-233-9

Query Match 100.0%; Score 514; DB 15; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATCTTTTGGTGAGCAACGGTTATTAGTGAAGATCAGAGATTTCAGA 60
Db |||||||
QY 848 GGACATCTTTTGGTGAGCAACGGTTATTAGTGAAGATCAGAGATTTCAGA 907
Db |||||||
QY 61 TGTGGTATGCCCTGGATGATGGATTTCCACTGGGTGATGAAGTATATCCAGAAAT 120
Db |||||||
QY 908 TGTGGTATGCCCTGGATGATGGATTTCCACTGGGTGATGAAGTATATCCAGAAAT 967
Db |||||||
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 180
Db |||||||
QY 968 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 1027
Db |||||||
QY 181 ATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db |||||||
QY 1028 ATGAAAAATGCTACTACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087
Db |||||||
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db |||||||
QY 1088 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1147
Db |||||||

QY 301 TTAAAGGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1148 TTAAAGGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207
QY 361 TTCTTACAAAACCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1208 TTCTTACAAAACCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1267
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACACACCAATCAACACATCATG 480
Db 1268 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACACACCAATCAACACATCATG 1327
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 3

US-10-406-156-9
; Sequence 9, Application US/10406156
; Publication No. US20030186421A1
; GENERAL INFORMATION:
; APPLICANT: Macphee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/406,156
; FILING DATE: 02-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,899
; FILING DATE: 12-May-2000
; APPLICATION NUMBER: 09/294,384
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 38..1360
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-406-156-9
Query Match 100.0%; Score 514; DB 16; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 848 GGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 907
QY 61 TGTGGTATGGCCCTGGATGGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 908 TGTGGTATGGCCCTGGATGGATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967
QY 121 CCTCAGCCCTCTTTTATCAAACTCTGAATATTTCCAAATATCTCTGCTAATATCATATAAA 180
Db 968 CCTCAGCCCTCTTTTATCAAACTCTGAATATTTCCAAATATCTCTGCTAATATCATATAAA 1027
QY 181 ATGAAAAAATGCTACTCCTCTGATAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1028 ATGAAAAAATGCTACTCCTCTGATAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1087
QY 241 CACCAGAAATTTTGTGCTGACTTCACCTTTTGGCAACTGGCAAAATAATTTGGACACATGCTCAAA 300
Db 1088 CACCAGAAATTTTGTGCTGACTTCACCTTTTGGCAACTGGCAAAATAATTTGGACACATGCTCAAA 1147
QY 301 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1148 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207
QY 361 TTCTTACAAAACCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1208 TTCTTACAAAACCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1267
QY 421 GGAGATGATGAGAATCTTAFTCCAGGGACCAACATTAACACCAATCAACACATCATG 480
Db 1268 GGAGATGATGAGAATCTTAFTCCAGGGACCAACATTAACACCAATCAACACATCATG 1327
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 4

US-09-962-832-110
; Sequence 110, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 110
; LENGTH: 1561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-110
Query Match 100.0%; Score 514; DB 9; Length 1561;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 1027 GGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 1086

QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 120
Db 1087 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 1146
QY 121 CCTCAGCCCTCTTTTATCAAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
Db 1147 CCTCAGCCCTCTTTTATCAAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 1206
QY 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1207 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1266
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1267 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1326
QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 360
Db 1327 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 1386
QY 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1387 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1446
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAAACAACCAATCAACACATCATG 480
Db 1447 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAAACAACCAATCAACACATCATG 1506
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1507 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1540

RESULT 5

US-10-741-601-89
; Sequence 89, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 1845
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-89

Query Match 99.8%; Score 513.2; DB 18; Length 1845;
Best Local Similarity 99.6%; Pred. No. 3.2e-127;
Matches 512; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTTCAGA 60
Db 989 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTTCAGA 1048
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT 120
Db 1049 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT 1108
QY 121 CCTCAGCCCTCTTTTATCAAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
Db 1109 CCTCAGCCCTCTTTTATCAAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 1168
QY 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1169 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1228

QY 241 CACCAGAAATTTTGTGACTTTCACATTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1229 CACCAGAAATTTTGTGACTTTCACATTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1288
QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 360
Db 1289 TTAAAGGGAGACATAGATTCAAATGVAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 1348
QY 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1349 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1408
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAAACAACCAATCAACACATCATG 480
Db 1409 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAAACAACCAATCAACACATCATG 1468
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1469 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1502

RESULT 6

US-10-741-601-90
; Sequence 90, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 1964
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-90

Query Match 99.8%; Score 513.2; DB 18; Length 1964;
Best Local Similarity 99.6%; Pred. No. 3.3e-127;
Matches 512; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTTCAGA 60
Db 1108 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTTCAGA 1167
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT 120
Db 1168 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT 1227
QY 121 CCTCAGCCCTCTTTTATCAAACTCTGAATATTTCCAATATCCTGCTAATATCATAAAA 180
Db 1228 CCTCAGCCCTCTTTTATCAAACTCTGAATATTTCCAATATCCTGCTAATATCATAAAA 1287
QY 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1288 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1347
QY 241 CACCAGAAATTTTGTGACTTTCACATTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1348 CACCAGAAATTTTGTGACTTTCACATTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1407
QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 360
Db 1408 TTAAAGGGAGACATAGATTCAAATGVAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 1467
QY 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1468 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1527
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAAACAACCAATCAACACATCATG 480

Db 1528 GGAGATGATGAGAACTCTTATTCAGGGACCAACATTAACACCAACCAATCAACACATCATG 1587
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 514
Db 1588 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1621

RESULT 7
US-10-415-682B-1
; Sequence 1, Application US/10415682B
; Publication No. US20040259087A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, David
; APPLICANT: McGinnis, Ralph
; APPLICANT: Spurr, Nigel
; APPLICANT: Valdes, Ana, Maria
; TITLE OF INVENTION: METHOD AND KIT TO DETERMINE LP-PLA2
; TITLE OF INVENTION: POLYMORPHIC VARIANTS ASSOCIATED WITH SUSCEPTIBILITY TO
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: P32704
; CURRENT APPLICATION NUMBER: US/10/415,682B
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: PCT/GB01/04876
; PRIOR FILING DATE: 2001-02-11
; PRIOR APPLICATION NUMBER: GB 0027181.7
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-415-682B-1

Query Match 99.8%; Score 513; DB 18; Length 1323;
Best Local Similarity 100.0%; Pred. No. 3.1e-127;
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGACATTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db 811 GGACATTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870
Qy 61 TGTGGTATTCGCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
Db 871 TGTGGTATTCGCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 930
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 180
Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 990
Qy 181 ATGAAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 991 ATGAAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1050
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACATGCTCAA 300
Db 1051 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACATGCTCAA 1110
Qy 301 TTAAGGGAGACATAGATTCAATATGAGCTATTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAGGGAGACATAGATTCAATATGAGCTATTTAGCAACAAAGCTTCATTAGCA 1170
Qy 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1230
Qy 421 GGAGATGATGAGAAATCTTATTCAGGGACCAACATTAACACCAACCAATCAACACATCATG 480
Db 1231 GGAGATGATGAGAAATCTTATTCAGGGACCAACATTAACACCAACCAATCAACACATCATG 1290
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 513

Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1323
RESULT 8
US-09-729-402-30
; Sequence 30, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,402
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20010021379A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-729-402-30

Query Match 99.7%; Score 512.4; DB 9; Length 1335;
Best Local Similarity 99.8%; Pred. No. 4.5e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db 811 GGACATTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870
Qy 61 TGTGGTATTCGCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
Db 871 TGTGGTATTCGCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 930
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 180
Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 990
Qy 181 ATGAAAAAATGCTACTACCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240

Db 991 ATGAAAAATGCTACTCACCTGATAAGAAAGAGATGATTACAATCAGGGTTCAGTC 1050
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCACTGCGCAAAATTAATTGGACACATGCTCAA 300
Db 1051 CACCAGAAATTTGCTGACTTCACTTTTGCACTGCGCAAAATTAATTGGACACATGCTCAA 1110
QY 301 TTAAGGGGAGACATAGATTCAATATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db 1111 TTAAGGGGAGACATAGATTCAATATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAACATTTAGGACTTCATAAAGATTTTGCAGTGGGACTGCTGATTGAA 420
Db 1171 TTCTTACAAAACATTTAGGACTTCATAAAGATTTTGCAGTGGGACTGCTGATTGAA 1230
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACACAAACCAATCAACACATCATG 480
Db 1231 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACACAAACCAATCAACACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 9
US-10-003-978A-30
; Sequence 30, Application US/10003978A
; Publication No. US20030072747A1
; GENERAL INFORMATION:
; APPLICANT: Couzens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, Gerstein & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6357
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/003,978A
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/729,402
; FILING DATE: 04-DEC-2000
; APPLICATION NUMBER: US 09/577,758
; FILING DATE: 23-MAY-2000
; APPLICATION NUMBER: US 09/010,715
; FILING DATE: 22-JAN-1998
; APPLICATION NUMBER: US 08/480,658
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030072747Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/37792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-003-978A-30
Query Match 99.7%; Score 512.4; DB 14; Length 1335;
Best Local Similarity 99.8%; Pred. No. 4.5e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 811 GGACATTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 870
QY 61 TGTGTTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 871 TGTGTTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 930
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAAATATCATATAAA 180
Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAAATATCATATAAA 990
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 991 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1050
QY 241 CACCAGAAATTTTGGTGGACTTTCACCTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 300
Db 1051 CACCAGAAATTTTGGTGGACTTTCACCTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA 1110
QY 301 TTAAGGGGAGACATAGATTCAAAATGAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db 1111 TTAAGGGGAGACATAGATTCAAAATGAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAACATTTAGGACTTCATAAAGATTTTGCAGTGGGACTGCTTGAATTGAA 420
Db 1171 TTCTTACAAAACATTTAGGACTTCATAAAGATTTTGCAGTGGGACTGCTTGAATTGAA 1230
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACACAAACCAATCAACACATCATG 480
Db 1231 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAACACAAACCAATCAACACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 10
US-10-172-118-1120
; Sequence 1120, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1120

```
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005084
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1120

Query Match      99.7%; Score 512.4; DB 17; Length 1505;
Best Local Similarity 99.8%; Pred. No. 4.8e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTCAGA 60
Db 972 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTCAGA 1031

QY 61 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 120
Db 1032 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 1091

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATCATAAAA 180
Db 1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATCATAAAA 1151

QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1152 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1212 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1271

QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1272 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1331

QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1332 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1391

QY 421 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAAACCAATCAACACATCATG 480
Db 1392 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAAACCAATCAACACATCATG 1451

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485
```

```
RESULT 11
US-10-342-887-1120
; Sequence 1120, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
```

```
; SEQ ID NO 1120
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005084
; DATABASE ENTRY DATE: 2001-06-18
US-10-342-887-1120

Query Match      99.7%; Score 512.4; DB 17; Length 1505;
Best Local Similarity 99.8%; Pred. No. 4.8e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTCAGA 60
Db 972 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAGATTCAGA 1031

QY 61 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 120
Db 1032 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 1091

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATCATAAAA 180
Db 1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATCATAAAA 1151

QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1152 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 300
Db 1212 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAAATTGGACACATGCTCAAA 1271

QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1272 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1331

QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1332 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1391

QY 421 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAAACCAATCAACACATCATG 480
Db 1392 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAACACAAACCAATCAACACATCATG 1451

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 12
US-10-755-889-277
; Sequence 277, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 277
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005084
; DATABASE ENTRY DATE: 2001-06-18
US-10-755-889-277

Query Match      99.7%; Score 512.4; DB 18; Length 1505;
Best Local Similarity 99.8%; Pred. No. 4.8e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAAGATCAGAGATTCAGA 60
Db 972 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAAGATCAGAGATTCAGA 1031
QY 61 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
Db 1032 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 1091
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180
Db 1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 1151
QY 181 ATGAAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1152 ATGAAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211
QY 241 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1212 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1271
QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGTATCTTAGCAACAACAAAGCTTCATTAGCA 360
Db 1272 TTAAAGGGAGACATAGATTCAAATGTAGCTATTGTATCTTAGCAACAACAAAGCTTCATTAGCA 1331
QY 361 TTCTTACAAAAGCATTTAGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1332 TTCTTACAAAAGCATTTAGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1391
QY 421 GGAGATGATGAGAATCTTATTTCCAGGGACCAACATTAACACAACCAATCAACACATCATG 480
Db 1392 GGAGATGATGAGAATCTTATTTCCAGGGACCAACATTAACACAACCAATCAACACATCATG 1451
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 13

US-09-729-402-7

; Sequence 7, Application US/09729402

; Patent No. US20010021379A1

; GENERAL INFORMATION:

; APPLICANT: Cousins, Lawrence S.

; Eberhardt, Christine D.

; Gray, Patrick W.

; Le Trong, Hai

; Tjoelker, Larry W.

; Wilder, Cheryl L.

; TITLE OF INVENTION: Platelet-Activating Factor

; Acetylhydrolase

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/729,402

; FILING DATE: 04-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/318,905

; FILING DATE: 06-OCT-1994

; APPLICATION NUMBER: US 08/133,803

; FILING DATE: 06-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: No. US20010021379Aland, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 27866/32793

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3658

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1520 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 162..1484

; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-729-402-7

Query Match 99.7%; Score 512.4; DB 9; Length 1520;

Best Local Similarity 99.8%; Pred. No. 4.8e-127;

Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAAGATCAGAGATTCAGA 60

Db 972 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTACTGAAGATCAGAGATTCAGA 1031

QY 61 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120

Db 1032 TGTGGTATTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 1091

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 180

Db 1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATAAAA 1151

QY 181 ATGAAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240

Db 1152 ATGAAAAAATGCTACTCCTGATATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211

QY 241 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300

Db 1212 CACCAGAAATTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1271

QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGTATCTTAGCAACAACAAAGCTTCATTAGCA 360

Db 1272 TTAAAGGGAGACATAGATTCAAATGTAGCTATTGTATCTTAGCAACAACAAAGCTTCATTAGCA 1331

QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420

Db 1332 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1391

QY 421 GGAGATGATGAGAATCTTATTTCCAGGGACCAACATTAACACAACCAATCAACACATCATG 480

Db 1392 GGAGATGATGAGAATCTTATTTCCAGGGACCAACATTAACACAACCAATCAACACATCATG 1451

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514

Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 14

US-10-003-978A-7

; Sequence 7, Application US/10003978A

; Publication No. US20030072747A1

; GENERAL INFORMATION:

; APPLICANT: Cousins, Lawrence S.

; Eberhardt, Christine D.

; Gray, Patrick W.

; Le Trong, Hai

; Tjoelker, Larry W.

; Wilder, Cheryl L.

;;
;; TITLE OF INVENTION: Platelet-Activating Factor
;; Acetylhydrolase
;;
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, Gerstein & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6357
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/003,978A
;; FILING DATE: 23-Oct-2001
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/729,402
;; FILING DATE: 04-DEC-2000
;; APPLICATION NUMBER: US 09/577,758
;; FILING DATE: 23-MAY-2000
;; APPLICATION NUMBER: US 09/010,715
;; FILING DATE: 22-JAN-1998
;; APPLICATION NUMBER: US 08/480,658
;; FILING DATE: 07-JUN-1995
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1994
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. US2003007274Aland, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/37792
;;
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;;
;; INFORMATION FOR SEQ ID NO: 7:
;;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1520 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 162..1484
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-003-978A-7

Query Match 99.7%; Score 512.4; DB 14; Length 1520;
Best Local Similarity 99.8%; Pred. No. 4.8e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
|||
DB 972 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 1031
|||
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
|||
DB 1032 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091
|||
QY 121 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCCTGCTAATATCATATAAA 180
|||
DB 1092 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCCTGCTAATATCATATAAA 1151
|||
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
|||
DB 1152 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211
|||
QY 241 CACCAGAAATTTTGCTGACTTCACTTTTGCAACTGGGCAAAATAATTGGACACATGCTCAAA 300
|||

Db 1212 CACCAGAAATTTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAAA 1271
|||
QY 301 TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 360
|||
DB 1272 TTAAAGGGAGACATAGATTCAAATGTAGCTATTGATCTTTAGCAACAAAGCTTCATTAGCA 1331
|||
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 420
|||
DB 1332 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 1391
|||
QY 421 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAAACAACCAATCAACACATCATG 480
|||
DB 1392 GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAAACAACCAATCAACACATCATG 1451
|||
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
|||
DB 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485
|||

RESULT 15
US-09-922-067-8
; Sequence 8, Application US/09922067
; Patent No. US20020177209A1
;
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
;
; TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
; Thereof And Use Of The Same In Diagnosis And Therapy
;
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,067
; FILING DATE: 03-Aug-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/193,130
; FILING DATE: 1998-11-17
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 572 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

; SEQUENCE DESCRIPTION: SEQ ID NO: 8:									
US-09-922-067-8									
Query Match 99.1%; Score 509.2; DB 9; Length 572;									
Best Local Similarity 99.4%; Pred. No. 2.2e-126;									
Matches 511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
QY	1	GGACATTC	TTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA	60					
Db	16	GGACATTC	TTTTAGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA	75					
QY	61	TGTGGTATT	GCCTGGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT	120					
Db	76	TGTGGTATT	GCCTGGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT	135					
QY	121	CCTCAGCCCT	CTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATATAAA	180					
Db	136	CCTCAGCCCT	CTTTTATCAACTCTGAATATTTCCAAATATCCTGCTAATATCATATAAA	195					
QY	181	ATGAAAAAAT	GTCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	240					
Db	196	ATGAAAAAAT	GTCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	255					
QY	241	CACCAGAA	TTTTGCTGACTTCACCTTTTGCACTGGCAAAATAATTGGACACATGCTCAA	300					
Db	256	CACCAGAA	TTTTGCTGACTTCACCTTTTGCACTGGCAAAATAATTGGACACATGCTCAA	315					
QY	301	TTAAAGGG	GAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA	360					
Db	316	TTAAAGGG	GAGACATAGATTCAATGTAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA	375					
QY	361	TTCTTACA	AAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA	420					
Db	376	TTCTTACA	AAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA	435					
QY	421	GGAGATGA	TGAGAAATCTTTATTCAGGGACCAACATTAAACAACCAATCAACACATCATG	480					
Db	436	GGAGATGA	TGAGAAATCTTTATTCAGGGACCAACATTAAACAACCAATCAACACATCATG	495					
QY	481	TTACAGAA	CTCTTCAGGAATAGAGAAATACAATT	514					
Db	496	TTACAGAA	CTCTTCAGGAATAGAGAAATACAATT	529					

Search completed: March 16, 2005, 06:35:28
Job time : 502.116 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:21 ; Search time 2076.29 Seconds
(without alignments)
9423.093 Million cell updates/sec

Title: US-09-922-067F-9_COPY_848_1361
Perfect score: 514
Sequence: 1 ggacattctttgtgggc.....aggaatagagaatacaatt 514

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514	100.0	560	4	BM788963
2	514	100.0	650	1	AI343491
3	514	100.0	734	6	CA312081
4	514	100.0	1326	9	AY407445
5	513	99.8	598	2	BF509203
6	510.8	99.4	1326	9	AY407446
7	504.4	98.1	1562	3	CR608325
8	503	97.9	1793	3	BC025674
9	499.4	97.2	1531	3	CR615354
10	498.6	97.0	1022	1	AL575852
11	497.4	96.8	519	2	AW071677
12	475.8	92.6	560	2	BF508812
13	467	90.9	505	5	BQ011547
14	465.8	90.6	818	5	BX330257
15	459	89.3	946	1	AL573565
16	412.2	80.2	900	4	BG530083
17	402	78.2	684	7	CK943719
18	398.8	77.6	677	7	CK950137
19	390.2	75.9	420	1	AA302965
20	384	74.7	689	5	BQ603958
21	383	74.5	619	7	CK953402
22	370	72.0	394	1	AI770111
23	364	70.8	593	7	CK954423
24	360.2	70.1	551	4	BM537293

C 25	354.2	68.9	405	6	CA436968	UI-H-DF1-
C 26	354	68.9	574	6	CB471515	sn40_A11.
C 27	350.6	68.2	622	4	BM536645	ha72f11.g
28	322.4	62.7	513	2	AW950435	EST362505
29	306	59.5	594	7	CK622757	mj01b04.y
30	306	59.5	1326	9	AY407447	Mus muscu
31	306	59.5	1695	3	AK005210	Mus muscu
32	306	59.5	1890	3	AK051454	Mus muscu
C 33	302.8	58.9	379	1	AA297235	EST112778
C 34	299.2	58.2	807	6	CA509646	UI-R-FS0-
35	298.6	58.1	508	1	AJ695792	AJ695792
36	297.2	57.8	798	7	CK129701	AGENCOURT
37	292.4	56.9	733	4	BI691924	BI691924
38	291.6	56.7	392	4	BI336794	AR081A11B
39	289.8	56.4	743	6	CD363890	UI-M-GL0-
40	288.4	56.1	678	6	CD364088	UI-M-GL0-
41	288.2	56.1	796	5	EX926110	EX926110
C 42	277.6	54.0	715	2	AW556825	L0273H05-
43	273.8	53.3	811	7	CK031981	AGENCOURT
C 44	273	53.1	542	7	CK953363	CK953363
45	272	52.9	914	7	CK023311	AGENCOURT

ALIGNMENTS

RESULT 1
BM788963
LOCUS
DEFINITION K-EST0068255 S19N665307 Homo sapiens CDNA clone S19N665307-2-H03
5', mRNA sequence.
ACCESSION BM788963
VERSION BM788963.1 GI:19137195
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: H column: 03
High quality sequence stop: 560.

FEATURES
source

Location/Qualifiers
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S19N665307-2-H03"
/sex="M"
/lab_host="Top10P"
/clone_lib="S19N665307"
/note="Organ: Stomach; Vector: pcns; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10f, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 514; DB 4; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.1e-123;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGCA 60
Db |||||||
QY 25 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGCA 84
Db |||||||
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAAAT 120
Db |||||||
QY 85 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAAAT 144
Db |||||||
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 180
Db |||||||
QY 145 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 204
Db |||||||
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTGAGTC 240
Db |||||||
QY 205 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTGAGTC 264
Db |||||||
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGGCAAAATATTTGGACACATGCTCAAA 300
Db |||||||
QY 265 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGGCAAAATATTTGGACACATGCTCAAA 324
Db |||||||
QY 301 TTAAGGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db |||||||
QY 325 TTAAGGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 384
Db |||||||
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGACTGGGACTGCTTGATTGAA 420
Db |||||||
QY 385 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGACTGGGACTGCTTGATTGAA 444
Db |||||||
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAAACACCAATCAACATCATG 480
Db |||||||
QY 445 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAAACACCAATCAACATCATG 504
Db |||||||
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db |||||||
QY 505 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 538
Db |||||||

RESULT 2
AI343491/c

LOCUS
DEFINITION
tb97c04.x1 NCI_CGAP Col6 Homo sapiens cDNA clone IMAGE:2062278 3', similar to SW:PAFA_HUMAN Q13093 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
AI343491
AI343491.1 GI:4080697
EST.
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 650)

REFERENCE
AUTHORS
TITLE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert length: 785 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 439.
Location/Qualifiers
1. .650
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2062278"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Col6"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 114584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

FEATURES

source

ORIGIN

Query Match 100.0%; Score 514; DB 1; Length 650;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGCA 60
Db |||||||
QY 544 GGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGCA 485
Db |||||||
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAAAT 120
Db |||||||
QY 484 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAAAT 425
Db |||||||
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTGCTAATATCATAAAA 180
Db |||||||
QY 424 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATATCTGCTAATATCATAAAA 365
Db |||||||
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTGAGTC 240
Db |||||||
QY 364 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTGAGTC 305
Db |||||||
QY 241 CACCAGAAATTTGCTGACTTCACCTTTGCAACTGGCAAAATATTTGGACACATGCTCAAA 300
Db |||||||
QY 304 CACCAGAAATTTGCTGACTTCACCTTTTGCACCTGGCAAAATATTTGGACACATGCTCAAA 245
Db |||||||
QY 301 TTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db |||||||
QY 244 TTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 185
Db |||||||
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGACTGGGACTGCTTGATTGAA 420
Db |||||||
QY 184 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGACTGGGACTGCTTGATTGAA 125
Db |||||||
QY 421 GGAGATGATGAGAATCTTATTTCCAGGGACCAACATTAAACACCAATCAACATCATG 480
Db |||||||
QY 124 GGAGATGATGAGAATCTTATTTCCAGGGACCAACATTAAACACCAATCAACATCATG 65
Db |||||||
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db |||||||
QY 64 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 31
Db |||||||

RESULT 3
CA312081/c

LOCUS

DEFINITION

UI-CF-FNO-afj-b-19-0-UI.81 UI-CF-FNO Homo sapiens cDNA clone

UI-CF-FNO-afj-b-19-0-UI 3', mRNA sequence.

ACCESSION
CA312081

734 bp mRNA linear EST 04-NOV-2002

VERSION	CA312081.1	GI:24530179	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 734)		
TITLE	Bonaldo,M.F., Lennon,G. and Soares,M.B.		
JOURNAL	Normalization and subtraction: two approaches to facilitate gene discovery		
MEDLINE	Genome Res. 6 (9), 791-806 (1996)		
PUBMED	97044477		
COMMENT	8889548		
	Contact: McCray, PB		
	McCray Lab.		
	University of Iowa		
	2024 University of Iowa Med Labs, Iowa City, IA 52242, USA		
	Tel: 319 356 4866		
	Fax: 319 356 7171		
	Email: paul-mccray@uiowa.edu		
	Tissue Procurement: Dr. M. J. Welsh, University of Iowa		
	cDNA Library preparation: Dr. M. Bento Soares, University of Iowa		
	cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).		
	The following repetitive elements were found in this cDNA sequence: 1-24, >AT rich#Low_complexity (matched complement)		
	Seq primer: M13 FORWARD		
	POLYA=Yes.		
FEATURES	Location/Qualifiers		
source	1..734		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="UI-CF-FNO-afj-b-19-0-UI"		
	/tissue_type="Human Lung Epithelial cells"		
	/lab_host="DH10B (Life Technologies) (T1 phage resistant)"		
	/clone_lib="UI-CF-FNO"		
	/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu		
	TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368		
	TAG LIB=UI-CF-FNO		
	TAG_SEQ=GGCTGTAGGC		
ORIGIN			
Query Match	100.0%;	Score 514;	DB 6; Length 734;
Best Local Similarity	100.0%;	Pred. No. 1.2e-123;	
Matches 514;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	GGACATTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA	60
Db	552	GGACATTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA	493
QY	61	TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT	120
Db	492	TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT	433
QY	121	CCTCAGCCCTCTTTTATCAACTCTGAATATTTCGAATATCTCGTAAATATCATATAAAA	180
Db	432	CCTCAGCCCTCTTTTATCAACTCTGAATATTTCGAATATCTCGTAAATATCATATAAAA	373
QY	181	ATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAAATCAGGGGTTTCAGTC	240
Db	372	ATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAAATCAGGGGTTTCAGTC	313
QY	241	CACCAGAAATTTTGCTGACTTTCACATTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA	300
Db	312	CACCAGAAATTTTGCTGACTTTCACATTTTGGCAACTGGCAAAATAATTGGACACATGCTCAA	253
QY	301	TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAAGCTTTCATTAGCA	360
Db	252	TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTTAGCAACAAAGCTTTCATTAGCA	193
QY	361	TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA	420
Db	192	TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA	133
QY	421	GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAAACACCAATCAACACATCATG	480
Db	132	GGAGATGATGAGAATCTTATTCCAGGGACCAACATTAAACACCAATCAACACATCATG	73
QY	481	TTACAGAACTCTTCAGGAATAGAGAAATACAATT	514
Db	72	TTACAGAACTCTTCAGGAATAGAGAAATACAATT	39
RESULT 4			
AY407445			
LOCUS	AY407445.1	GI:39763416	
DEFINITION	Homo sapiens PLA2G7 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY407445		
VERSION	AY407445.1	GI:39763416	
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1326)		
	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science 302 (5652), 1960-1963 (2003)		
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1326)		
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..1326		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
	<1..>1326		
	/gene="PLA2G7"		
	/locus_tag="HCM2893"		
ORIGIN			
Query Match	100.0%;	Score 514;	DB 9; Length 1326;
Best Local Similarity	100.0%;	Pred. No. 1.4e-123;	
Matches 514;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	GGACATTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA	60
Db	811	GGACATTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA	870
QY	61	TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT	120
Db	871	TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAATT	930

QY 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 180
Db 931 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATAAAA 990
QY 181 ATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 991 ATGAAAAAATGCTACTCACCTGTATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1050
QY 241 CACCAGAAATTTTGTGCTGACTTCACTTTTGCAACTGGCAAAATTAATTGGACACATGCTCAAA 300
Db 1051 CACCAGAAATTTTGTGCTGACTTCACTTTTGCAACTGGCAAAATTAATTGGACACATGCTCAAA 1110
QY 301 TTAAGGGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAGGGGAGACATAGATTCAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAGATTTTGTATCATGCTGGGACTGCTTGATTGAA 420
Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAGATTTTGTATCATGCTGGGACTGCTTGATTGAA 1230
QY 421 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACTCAACACATCATG 480
Db 1231 GGAGATGATGAGAATCTTATTCAGGGACCAACATTAACACAACTCAACACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 5
BF509203/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html The following repetitive
elements were found in this cDNA sequence: 1-23,
>AT-rich#Low complexity
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
source
1. .598
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3086345"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP Sub8"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; NCI CGAP Sub8
is a substracted library derived from NCI CGAP Sub5. The
NCI CGAP Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub5 was used

as a tracer in a subtractive hybridization with a driver
comprising: a pool of clones from NCI CGAP Sub5 (IMAGE
clone Ids 2732833-2737415, 3068040-3069191; 25% of the
driver population), a pool of clones from NCI CGAP Sub4
(IMAGE clone Ids 2723592-2729326; 25% of the driver
population), NCI CGAP Sub6 (pool AIF-AJU, IMAGE Ids
2728969-2733190; 25% of the driver population), and
NCI CGAP Sub7 (IMAGE Ids 3069192-3072238,
3081864-3084550; 25% of the driver population).
Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
Genome Research 6, 791-806.
TAG_TISSUE=leiomyosarcoma
TAG_LIB=NCI CGAP_Lei2
TAG_SEQ=AATCG"

ORIGIN

Query Match 99.8%; Score 513; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.1e-123;
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GACATTCTTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGAT 61
Db 550 GACATTCTTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGAT 491
QY 62 GTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATTC 121
Db 490 GTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATTC 431
QY 122 CTCAGCCCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTGCTAATATCATAAAA 181
Db 430 CTCAGCCCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTGCTAATATCATAAAA 371
QY 182 TGA AAAAATGCTACTACCTGATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTCC 241
Db 370 TGA AAAAATGCTACTACCTGATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTCC 311
QY 242 ACCAGAAATTTTGTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAAT 301
Db 310 ACCAGAAATTTTGTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAAT 251
QY 302 TAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCAT 361
Db 250 TAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCAT 191
QY 362 TCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAAG 421
Db 190 TCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAAG 131
QY 422 GAGATGATGAGAATCTTATTCAGGGACCAACATTAAACACAAACCAATCAACACATCATGT 481
Db 130 GAGATGATGAGAATCTTATTCAGGGACCAACATTAAACACAAACCAATCAACACATCATGT 71
QY 482 TACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 70 TACAGAACTCTTCAGGAATAGAGAAATACAATT 38

RESULT 6
AY407446
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
Pan troglodytes PLA2G7 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY407446
AY407446.1 GI:39763417
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1326)
Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,

Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1326)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
1..1326
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1326
/gene="PLA2G7"
/locus_tag="HCW2893"
ORIGIN
Query Match 99.4%; Score 510.8; DB 9; Length 1326;
Best Local Similarity 99.6%; Pred. No. 9.3e-123;
Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGACATTCCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db 811 GGACATTCCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 870
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 871 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 930
QY 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAA 180
Db 931 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAA 990
QY 181 ATGAAAAAATGCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 991 ATGAAAAAATGCTACTCACCTGATAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1050
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGGCAAAATAATTTGGACACATGCTCAAA 300
Db 1051 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGGCAAAATAATTTGGACACATGCTCAAA 1110
QY 301 TTAAAGGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAAGGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1230
QY 421 GGAGATGATGAGAAATCTTATTCAGGGGACCAACATTAACACACCAATCAACACATCATG 480
Db 1231 GGAGATGATGAGAAATCTTATTCAGGGGACCAACATTAACACACCAATCAACACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324
RESULT 7
CR608325 1562 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0D1067YM18 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).

ACCESSION CR608325
VERSION CR608325.1 GI:50489132
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1562)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1562)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source Location/Qualifiers
1..1562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1067YM18"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 98.1%; Score 504.4; DB 3; Length 1562;
Best Local Similarity 99.8%; Pred. No. 4.6e-121;
Matches 505; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACATTCCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
Db 1057 GGACATTCCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 1116
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1117 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1176
QY 121 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAA 180
Db 1177 CCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAA 1236
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1237 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1296
QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACATGCTCAAA 300
Db 1297 CACCAGAAATTTGCTGACTTCACTTTTGCAACTGGCAAAATAATTTGGACACATGCTCAAA 1356
QY 301 TTAAAGGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1357 TTAAAGGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1416
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 420
Db 1417 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAA 1476
QY 421 GGAGATGATGAGAAATCTTATTCAGGGGACCAACATTAACACACCAATCAACACATCATG 480
Db 1477 GGAGATGATGAGAAATCTTATTCAGGGGACCAACATTAACACACCAATCAACACATCATG 1536
QY 481 TTACAGAACTCTTCAGGAATAGAGAA 506
|||||

DEFINITION. ws53b01.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2500873 3' similar to SW_PAPA_HUMAN Q13093 PLATELET-ACTIVATING FACTOR ACETYLDHROLASE PRECURSOR ;, mRNA sequence.

AW071677

AW071677.1 GI:6026675

EST.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 519)

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 461.

Location/Qualifiers

1. 519

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2500873"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/clone_lib="NCI CGAP Brn25"

/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATAGGTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 96.8%; Score 497.4; DB 2; Length 519;

Best Local Similarity 99.8%; Pred. No. 2.5e-119;

Matches 498; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGATGTGGTATTGCCCTG 75

DB 519 GGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGATGTGGTATTGCCCTG 460

QY 76 GATGCATGATGTTTCCACTGGGTGATGAAGTATATCCAGAATTCCTCAGCCCTCTTT 135

DB 459 GATGCATGATGTTTCCACTGGGTGATGAAGTATATCCAGAATTCCTCAGCCCTCTTT 400

QY 136 TTTATCACTCTGAATATTTCCAAATATCTGCTAATATCATATAAAATGAAAAATGCTAC 195

DB 399 TTTATCACTCTGAATATTTCCAAATATCTGCTAATATCATATAAAATGAAAAATGCTAC 340

QY 196 TCACCTGATAAAGAAAGAAAGATGATTACATCAGGGGTTTCAGTCCACAGAAATTTGCT 255

DB 339 TCACCTGATAAAGAAAGAAAGATGATTACATCAGGGGTTTCAGTCCACAGAAATTTGCT 280

QY 256 GACTTCACCTTTGCAACTGGCAAAATAATTGGACACATGCTCAAAATTAAGGGAGACATA 315

DB 279 GACTTCACCTTTGCAACAGGCAAAATAATTGGACACATGCTCAAAATTAAGGGAGACATA 220

QY 316 GATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTTCATTAGCATTTTACAAAAGCAT 375

DB 219 GATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTTCATTAGCATTTTACAAAAGCAT 160

QY 376 TTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAAGGAGATGATGAGAAT 435

DB 159 TTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGAAGGAGATGATGAGAAT 100

QY 436 CTTATTCCAGGACCAACATTTAAACACACCAATCAACACATCATGTTACAGAACTCTTCA 495

DB 99 CTTATTCCAGGACCAACATTTAAACACACCAATCAACACATCATGTTACAGAACTCTTCA 40

QY 496 GGAATAGAGAAATACAATT 514

DB 39 GGAATAGAGAAATACAATT 21

RESULT 12

BF508812/c

LOCUS

DEFINITION

UI-H-BI4-aor-b-03-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085757 3', mRNA sequence.

BF508812

BF508812.1 GI:11592110

EST.

Source

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 560)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1. 560

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3085757"

/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI_CGAP Sub8"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; NCI_CGAP Sub8 is a subtracted library derived from NCI_CGAP_Sub5. The NCI_CGAP Sub8 library had 2.5 million recombinants. A single-stranded DNA preparation of NCI_CGAP_Sub5 was used as a tracer in a subtractive hybridization with a driver comprising: a pool of clones from NCI_CGAP_Sub5 (IMAGE clone Ids 2732833-2737415, 3068040-3069191; 25% of the driver population), a pool of clones from NCI_CGAP_Sub4 (IMAGE clone Ids 2723592-2729326; 25% of the driver population), NCI_CGAP_Sub6 (pool AIF-AJU, IMAGE Ids 2728969-2733190; 25% of the driver population), and NCI_CGAP_Sub7 (IMAGE Ids 3069192-3072238, 3081864-3084550; 25% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806. TAG_TISSUE=leiomyosarcoma TAG_LIB=NCI_CGAP_Lei2

FEATURES

source

FEATURES
source
 Location/Qualifiers
 1..505
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-1-BC1p-asi-a-06-0-UI"
 /tissue_type="Placenta"
 /dev_stage="8-9 weeks"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Pl3"
 /note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP Pl3 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are GA, AGGA. For additional information, contact: Bento Soares, bento-soares@uiowa.edu
 TAG_TISSUE=placenta human 8 week
 TAG_LIB=UI-1-BC1p
 TAG_SEQ=GA"

ORIGIN
 Query Match 90.9%; Score 467; DB 5; Length 505;
 Best Local Similarity 100.0%; Pred. No. 2.2e-111;
 Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	48	TCAGAGATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGT	107
DB	505	TCAGAGATTCAGATGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGT	446
QY	108	ATATTCCAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGC	167
DB	445	ATATTCCAGAAATTCCTCAGCCCCCTCTTTTATCAACTCTGAATATTTCCAATATCCTGC	386
QY	168	TAATATCATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAAT	227
DB	385	TAATATCATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAAT	326
QY	228	CAGGGGTTTCAGTCCACCAGAAATTTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGG	287
DB	325	CAGGGGTTTCAGTCCACCAGAAATTTTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGG	266
QY	288	ACACATGCTCAAATTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACA	347
DB	265	ACACATGCTCAAATTAAGGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACA	206
QY	348	AGCTTCATTAGCATTCITACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGA	407
DB	205	AGCTTCATTAGCATTCITACAAAAGCATTTAGGACTTCATAAAGATTTTGATCAGTGGA	146
QY	408	CTGCTTGATTGAAGGAGATGATGAGAAATCTTATCCAGGGACCAACATTAAACACAACCA	467
DB	145	CTGCTTGATTGAAGGAGATGATGAGAAATCTTATCCAGGGACCAACATTAAACACAACCA	86
QY	468	TCAACACATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT	514
DB	85	TCAACACATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT	39

RESULT 14
 BX330257/c
 LOCUS
 DEFINITION
 clone CS0D1034YP21 3-PRIME, mRNA sequence.
 ACCESSION
 VERSION
 BX330257.2 GI:46267134

ORIGIN		TAG_SEQ=AATCG			
Query Match		92.6%	Score 475.8;	DB 2;	Length 560;
Best Local Similarity		96.5%	Pred. No. 1.1e-113;		
Matches 497;		Conservative	0;	Mismatches 17;	Indels 1; Gaps 1;
QY	1	GGACATTC	TTTTGGTGGAGCAACGGTTATTT	CAGACTCTTTAGTGAAGATCAGAGATTCAGA	60
DB	552	GGACATTC	TTTTGGTGGAGCAACGGTTATTT	CAGACTCTTTAGTGAAGATCAGAGATTCAGA	493
QY	61	TGTGGTATT	GGCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAATT	120	
DB	492	TGTGGTATT	GGCCTGGATGCATGGATGTTTCCACTGGGTGATGACGTATATTTCCAGAATT	433	
QY	121	CCTCAGCCCTCT	TTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAAA	180	
DB	432	CCTCAGCCCTCT	TTTTTATCAACTATGAATATTTACCAATATCTGGTAATATCATATAAAA	373	
QY	181	ATGAAAAAATGCTACT	CACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	240	
DB	372	ATGAAAAAATGCTACT	CACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	313	
QY	241	CACCAGAAATTTTGCTGACTT	CACTTTTGCAACTGGCAAAATAATTTGGACAC-ATGCTCAA	299	
DB	312	CACCAGAAATTTTGCTGACTT	CACTTTTGCAACTGGCAAAATAATTTGGACACGATGCTCAA	253	
QY	300	ATTAAAGGGAGACATAGATT	CAAAATGCAGCTATTGATCTTTAGCAACAAAGCTTTCATTAGC	359	
DB	252	ATTAAAGGGAGACATAGATT	CAAAATGCATCTATTGATTTTGTAGCAACAAAGCTTTCATTAGC	193	
QY	360	ATTCTTACAAAAGCATT	TTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGA	419	
DB	192	ATTCTTACAAAAGCATT	TTAGGACTTCATAAAGATTTTGATCAGTGGGACTGCTTGATTGA	133	
QY	420	AGGAGATGATGAGAATCTT	TATTCAGGGACCAACATTAAACAACCAATCAACACATCAT	479	
DB	132	AGGAGATGATGAGAATCTT	TATTCAGGGACCAACATTAAACAACCAATCAACACATCAT	73	
QY	480	GTTACAGAATCTTTCAGGAAT	TAGAGAAATACAAATT	514	
DB	72	ATTACAGAATCTTTCAGGAAT	TAGAGAAATACAAATT	38	
<p>RESULT 13</p> <p>BQ011547/c</p> <p>LOCUS</p> <p>DEFINITION</p> <p>UI-1-BC1p-asi-a-06-0-UI.s1 NCI_CGAP_P13 Homo sapiens cDNA clone</p> <p>UI-1-BC1p-asi-a-06-0-UI 3', mRNA sequence.</p> <p>BQ011547</p> <p>BQ011547.1 GI:19736448</p> <p>EST.</p> <p>SOURCE</p> <p>Homo sapiens (human)</p> <p>ORGANISM</p> <p>Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 (bases 1 to 505)</p> <p>NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.</p> <p>National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index</p> <p>Unpublished (1997)</p> <p>Contact: Robert Strausberg, Ph.D.</p> <p>Email: cgapbs-r@mail.nih.gov</p> <p>Tissue Procurement: Dr. Steven Brown</p> <p>cDNA Library preparation: Dr. M. Bento Soares, University of Iowa</p> <p>cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa</p> <p>DNA Sequencing by: Dr. M. Bento Soares, University of Iowa</p> <p>Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu</p> <p>The following repetitive elements were found in this cDNA sequence: 1-24, >AT rich#Low_complexity (matched complement)</p> <p>Seq primer: M13 FORWARD</p> <p>POLYA=Yes.</p>					

```
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 818)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 1, 2003 this sequence version replaced gi:30311923.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2019.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAK056DG02NM1&c=2019.r.
Location/Qualifiers
1. 818
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI034YP21"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES
source
Query Match 90.6%; Score 465.8; DB 5; Length 818;
Best Local Similarity 96.4%; Pred. No. 5.1e-111;
Matches 487; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
DB 542 GGGCATTCCTTTATGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 483
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATATCCAGAATT 120
DB 482 TGTGGTAATGCCCTGGATGCATGGATGTTTCCGCTGGTCTGAAGTATATCCAGAAGT 423
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 180
DB 422 CCTCAGCCCTCTTTTATCAACTCTGAATATGTGCAATATCTGCTAATATCATATAA 363
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTCAGTC 240
DB 362 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTCAGTC 303
QY 241 CACCAGAATTTTGTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
DB 302 CACCAGAATTTTGTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 243
QY 301 TTAAAGGGGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
DB 242 TTAAAGGGGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 183
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTTGATGAA 420
DB 182 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGGATCAGTGGGACTGCTTGATGAA 123
QY 421 GGAGATGATGAGAATCTTTATCCAGGGACCAACATTAAACAACCAATCAACACATCATG 480
DB 122 GGAGATGATGAGAATCTTTATGCCAGGGACCAACATTAAACAACCAATCAACACATC-TG 64
QY 481 TTACAGAACTCTTCAGGAATAGAGA 505
```

```
Db 63 TTACAGAACTCTCAGGAAGAGAGAAA 39

RESULT 15
AL573565/c
LOCUS
DEFINITION
AL573565 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI049YE02 3-PRIME, mRNA sequence.
ACCESSION
AL573565
VERSION
AL573565.2 GI:31294910
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 16, 2001 this sequence version replaced gi:12932922.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3382.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI049BC01NP1&c=3382.r.
Location/Qualifiers
1. 946
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI049YE02"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 89.3%; Score 459; DB 1; Length 946;
Best Local Similarity 92.4%; Pred. No. 3.2e-109;
Matches 463; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 1 GGACATTCCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
DB 501 GGACAGTCTTTGGTGGAGCAACGGTTATTCAGACTCTTRGTGAAGATCAGAGATTCAGA 442
QY 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATCCAGAATT 120
DB 441 TGTGGTATTGCCCKGGATGCATGGATGTTSCCACTGGGTGATGAAGTATATCCAGAATT 382
QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTAATATCATATAA 180
DB 381 CCTCAGCCCTCTTTTATCAACCCYGAATATCCCCAATACCCYGCMAATATCATATAA 322
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTCAGTC 240
DB 321 AKGMAAAATGCMCTCMCTGTATAAAGAAAGAAAGATGATSACATCAGGGGCTCAGCC 262
QY 241 CACCAGAATTTTGTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAA 300
DB 261 CMCCAGAATTTTGTGACTTCACCTTTTGCAACTGGCAAAAGAAATTGGACACATGCTCAA 202
QY 301 TTAAAGGGGACATAGATTCAAATSCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
```

```

Db      201 TTAAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 142
Qy      361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTGATCAGTGGGACTGCTTGATTGAA 420
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      141 TTCTTWTAAATKCAATTTAGGACHTCATAATGATTTGWTCAGTGGGACTGCTTGATTGAA 82
Qy      421 GGAGATGATGAGAAATCTTATTCCAGGGGACCAACATTAACACCAATCAACACATCATG 480
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      81 GGAGATGATGARAATCTTATTCCAGGGGCCAACATTAAYACACCAATCAACACTTCWTG 22
Qy      481 TTACAGAACTCTTCAGGAATA 501
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      21 TTACAGAACTCTTCAGGAATA 1

```

Search completed: March 15, 2005, 18:21:48
 Job time : 2080.29 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 09:47:50 ; Search time 165.735 Seconds
(without alignments)
1029.119 Million cell updates/sec

Title: US-09-922-067F-14
Perfect score: 2358
Sequence: 1 MVPPKLVLFCLGCLAVVY.....INTTQHIMLQNSSGIEKYN 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2358	100.0	441	3 AAB01942	Aab01942 Human low
2	2358	100.0	441	5 AAE14750	Aae14750 Human lip
3	2358	100.0	442	2 AAR64928	Aar64928 Human T-C
4	2354	99.8	441	2 AAR71913	Aar71913 Human pla
5	2354	99.8	441	2 AAW23796	Aaw23796 Human pla
6	2354	99.8	441	2 AAW09808	Aaw09808 Platelet-
7	2354	99.8	441	2 AAW26498	Aaw26498 Human pla
8	2354	99.8	441	2 AAW38361	Aaw38361 Human pla
9	2354	99.8	441	2 AAW96334	Aaw96334 Human pla
10	2354	99.8	441	2 AAW73359	Aaw73359 Human PAF
11	2354	99.8	441	3 AAY88301	Aay88301 Human pla
12	2354	99.8	441	3 AAY50735	Aay50735 Human PAF
13	2354	99.8	441	3 AAB07774	Aab07774 Plasma pl
14	2354	99.8	441	4 AAE00761	Aae00761 Human pla
15	2354	99.8	441	4 AAB49451	Aab49451 Platelet-
16	2354	99.8	441	4 AAE15507	Aae15507 Human pla
17	2354	99.8	441	5 ABG61862	Abg61862 Prostate
18	2354	99.8	441	6 ABP55072	Abp55072 Human lip
19	2354	99.8	441	6 ADA19491	Ada19491 Human pla
20	2354	99.8	441	7 ADP65141	Adp65141 Human pho
21	2354	99.8	441	8 ADJ57408	Adj57408 Human pho
22	2354	99.8	441	8 ADP12938	Adp12938 Protein e
23	2354	99.8	441	8 ADR14277	Adr14277 Human NF-
24	2354	99.8	441	8 ADR51543	Adr51543 Human lip
25	2354	99.8	441	8 ADP54611	Adp54611 Human PRO

26	2354	99.8	441	8 ADP23967	Adp23967 PRO polyp
27	2351	99.7	441	2 AAR71920	Aar71920 Human ace
28	2351	99.7	441	2 AAR71921	Aar71921 Human ace
29	2351	99.7	441	4 AAE00768	Aae00768 Human pla
30	2351	99.7	441	4 AAE00769	Aae00769 Human pla
31	2351	99.7	441	4 AAE15515	Aae15515 Human pla
32	2351	99.7	441	4 AAE15516	Aae15516 Human pla
33	2349	99.6	441	4 AAE00771	Aae00771 Human pla
34	2349	99.6	441	4 AAE15518	Aae15518 Human pla
35	2346	99.5	441	2 AAR71923	Aar71923 Human ace
36	2346	99.5	441	2 AAR71922	Aar71922 Human ace
37	2346	99.5	441	4 AAE00770	Aae00770 Human pla
38	2346	99.5	441	4 AAE00773	Aae00773 Human pla
39	2346	99.5	441	4 AAE00774	Aae00774 Human pla
40	2346	99.5	441	4 AAE00772	Aae00772 Human pla
41	2346	99.5	441	4 AAE15519	Aae15519 Human pla
42	2346	99.5	441	4 AAE15517	Aae15517 Human pla
43	2346	99.5	441	4 AAE15520	Aae15520 Human pla
44	2346	99.5	441	4 AAE15521	Aae15521 Human pla
45	2344	99.4	441	2 AAR71924	Aar71924 Human ace

ALIGNMENTS

RESULT 1
AAB01942
ID AAB01942 standard; protein; 441 AA.
XX

AC AAB01942;

DT 18-SEP-2000 (first entry)

DE Human low density lipoprotein-associated phospholipase A2 (LDL-PLA2).

KW Human; low density lipoprotein associated phospholipase A2; LDL-PLA2;
KW plasma PAF acetyl hydroxylase; recombinant; purification;
KW short chain phospholipid; serine-dependant phospholipase; inflammation;
KW proinflammatory; anti inflammatory; drug screening; antibody; diagnosis.

XX Homo sapiens.

PN WO200024910-A1.

PD 04-MAY-2000.

PF 27-OCT-1999; 99WO-GB003551.

PR 28-OCT-1998; 98GB-00023647.

PR 28-OCT-1998; 98GB-00023648.

PA (SMIK) SMITHKLINE BEECHAM PLC.

PI Boyd H, Tew DG;

DR WPI; 2000-350749/30.

DR N-PSDB; AAA52357.

XX
PT Recombinant low density lipoprotein associated phospholipase A2, used to produce antibodies for diagnostics, is purified using a Blue Sepharose and Q Sepharose column.

PS Claim 6b; Page 17; 28pp; English.

XX
CC The present sequence represents human LDL-PLA2. The invention relates to a method for purifying recombinant low density lipoprotein- associated phospholipase A2 (LDL-PLA2). The method comprises applying a cell extract, supernatant or solution containing the recombinantly expressed LDL-PLA2 to a zinc chelating column, applying the eluate to a Blue Sepharose column, and applying that eluate to a Q Sepharose column. The invention also provides a process which additionally comprises the prior steps of constructing a vector comprising a cDNA encoding a histidine tagged LDL-PLA2 or fragment thereof, expressing the tagged protein in a

ID XX AAR64928 standard; protein; 442 AA.
AC AAR64928;
XX
DT 25-MAR-2003 (revised)
DT 18-AUG-1995 (first entry)
XX
DE Human T-cell lymphoma lipoprotein-associated phospholipase-A2.
XX
KW T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2; enzyme;
KW atherosclerosis; diagnosis; therapy; antiarteriosclerotic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 25..31
FT Peptide /note= "Peptide 4"
FT Peptide 115..133
FT Peptide /note= "Peptide 3"
FT Peptide 298..327
FT Peptide /note= "Peptide 2"
FT Peptide 368..393
FT Peptide /note= "Peptide 1"
XX
PN WO9500649-A1.
XX
PD 05-JAN-1995.
XX
PF 24-JUN-1994; 94WO-GB001374.
XX
PR 25-JUN-1993; 93GB-00013144.
PR 11-JAN-1994; 94GB-00000413.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Macphee CH, Tew DG, Southan CD, Hickey DMB, Gloger IS;
PI Lawrence GMP, Rice SQJ;
XX
DR WPI; 1995-052086/07.
DR N-PSDB; AAQ81780.
XX
PT Purified lipoprotein associated phospholipase A2 - used to develop prods.
PT for diagnosis and therapy, partic. inhibitors for treatment of
PT atherosclerosis.
XX
PS Claim 8; Page 19; 29pp; English.
XX
CC This sequence encodes an enzyme which may be used in a method of
CC screening compounds to identify those compounds which inhibit Lp-PLA2
CC which involves contacting isolated Lp-PLA2 with a test compound and
CC measuring the rate of turnover of an enzyme substrate as compared with
CC the rate of turnover in the absence of the test compound. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
SQ Sequence 442 AA;
Query Match 100.0%; Score 2358; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 4.5e-218;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPPKLVFLFCGCLAVVYFDPDQYINPVAMKSSAWVNIQVLMMAAFSGQTKIPRGN 60
Db 1 MPPKLVFLFCGCLAVVYFDPDQYINPVAMKSSAWVNIQVLMMAAFSGQTKIPRGN 60
QY 61 GPYVSGCTDLMFDHTNKGTFRLYYPSPQDNDRDLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYVSGCTDLMFDHTNKGTFRLYYPSPQDNDRDLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFLGSMTPANWNSPLRPGKYPVLVVFHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFLGSMTPANWNSPLRPGKYPVLVVFHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSASATYFKDQSAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILID 240

Db 181 DRSASATYFKDQSAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQTLSEDRFCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQTLSEDRFCGIALDAWMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYANIKMKCYSPDKERKMITIRGSHQNFADTFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYANIKMKCYSPDKERKMITIRGSHQNFADTFA 360
QY 361 TGIIGHMLKLKGDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGIIGHMLKLKGDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441
RESULT 4
AAR71913
ID AAR71913 standard; protein; 441 AA.
XX
AC AAR71913;
XX
DT 25-MAR-2003 (revised)
DT 05-DEC-1995 (first entry)
XX
DE Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).
XX
KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9509921-A1.
XX
PD 13-APR-1995.
XX
PF 06-OCT-1994; 94WO-US011340.
XX
PR 06-OCT-1993; 93US-00133803.
XX
PA (ICOS-) ICOS CORP.
XX
PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
XX
DR WPI; 1995-155262/20.
DR N-PSDB; AAQ87947.
XX
PT New nucleic acid encoding platelet activating factor, acetyl:hydrolase -
PT useful in diagnosis and for treating inflammatory diseases, e.g.
PT pleurisy.
XX
PS Claim 5; Page 53-54; 88pp; English.
XX
CC The human acetyl hydrolase gene (AAQ87947) has been isolated and
CC purified. The platelet activating factor acetyl hydrolase (AAR71913) is
CC useful in the treatment of inflammatory diseases, in particular pleurisy,
CC asthma, rhinitis and eczema. The gene may also be used in raising
CC monoclonal antibodies specific for PAF-AH that are useful in the
CC diagnosis of such diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 441 AA;
Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 1.1e-217;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPPKLVFLFCGCLAVVYFDPDQYINPVAMKSSAWVNIQVLMMAAFSGQTKIPRGN 60

Db 1 MVPKHLVLCGCLAVVYFDFWQYINPVAMKSSAWVNIQVLMMAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMPDHTNKGFLRLYYPSQNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMPDHTNKGFLRLYYPSQNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFGSMTTPANNWNSPLRPEGEKYLPLVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTTPANNWNSPLRPEGEKYLPLVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRASATYFVKDQSAAEIGDKSWLYLRLTKQEEETHIRNEQVRQRAKECSQALSILIDID 240
Db 181 DRASATYFVKDQSAAEIGDKSWLYLRLTKQEEETHIRNEQVRQRAKECSQALSILIDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRCGIALDAWMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
QY 361 TGKIIIGHMLKLGDIIDSNAAIDLSNKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLGDIIDSNVAIDLSNKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 5
AAW23796
ID AAW23796 standard; protein; 441 AA.

AC AAW23796;
XX 25-MAR-2003 (revised)
DT 04-NOV-1997 (first entry)
XX Human plasma platelet activating factor acetylhydrolase.
DE Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;
XX pro-inflammatory arachidonic acid metabolite; reperfusion injury;
KW central nervous system shock; arthritis; Crohn's disease;
KW systemic lupus erythematosus; adult respiratory distress syndrome.
XX Homo sapiens.
OS US5641669-A.
XX 24-JUN-1997.
XX 06-OCT-1994; 94US-00318905.
XX 06-OCT-1993; 93US-00133803.
PA (ICOS-) ICOS CORP.
XX Tjoelker LW, Trong HL, Cousens LS, Wilder CL, Eberhardt CD;
PI Gray P;
XX WPI; 1997-340947/31.
DR N-PSDB; AAT80564.
XX New human plasma platelet activating factor acetylhydrolase - useful as
PT anti-inflammatory for treatment of asthma, anaphylaxis, shock, etc.
XX Claim 1; Col 35-38; 43pp; English.
XX The present sequence represents the purified and isolated human plasma
CC platelet activating factor acetylhydrolase (PAF-AH). This novel
CC polypeptide inactivates PAF and oxidatively fragmented phospholipids such

CC as pro-inflammatory arachidonic acid metabolites, and so can be used to
CC treat inflammation by augmenting endogenous activity. Typical
CC applications are in asthma, anaphylaxis, shock, reperfusion injury,
CC central nervous system shock, arthritis, Crohn's disease, systemic lupus
CC erythematosus, adult respiratory distress syndrome. The polypeptide can
CC also be used to raise specific antibodies (Ab) which are useful as
CC immunoassay reagents and for generating anti-idiotypic antibodies. The
CC nucleic acid encoding the protein can be used to screen for related genes
CC ; in hybridisation assays to assess the protein- producing cells; to
CC generate knockout mice; to detect genetic mutations and (antisense
CC sequences) to inhibit the protein expression. Unlike PAF receptor
CC antagonists, the protein is a natural component of plasma. (Updated on 25
CC -MAR-2003 to correct pf field.)
XX
SQ Sequence 441 AA;

Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 1.1e-217;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MVPKHLVLCGCLAVVYFDFWQYINPVAMKSSAWVNIQVLMMAASFGQTKIPRGN 60
Db 1 MVPKHLVLCGCLAVVYFDFWQYINPVAMKSSAWVNIQVLMMAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMPDHTNKGFLRLYYPSQNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMPDHTNKGFLRLYYPSQNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFGSMTTPANNWNSPLRPEGEKYLPLVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTTPANNWNSPLRPEGEKYLPLVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRASATYFVKDQSAAEIGDKSWLYLRLTKQEEETHIRNEQVRQRAKECSQALSILIDID 240
Db 181 DRASATYFVKDQSAAEIGDKSWLYLRLTKQEEETHIRNEQVRQRAKECSQALSILIDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRCGIALDAWMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
QY 361 TGKIIIGHMLKLGDIIDSNAAIDLSNKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLGDIIDSNVAIDLSNKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 6
AAW09808
ID AAW09808 standard; protein; 441 AA.

XX AAW09808;
XX 25-MAR-2003 (revised)
DT 12-JUN-1997 (first entry)
XX Platelet-activating factor acetylhydrolase.
DE Human platelet-activating factor acetylhydrolase; PAF-AH; detection;
KW mutation; V279F; substitution; restriction fragment length polymorphism;
KW analysis; diagnosis; inherited; deficiency; severe respiratory symptom;
KW asthmatic children; treat; inflammatory condition.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1. .41

FT FT /label= signal_peptide
FT /note= "possibly contains additional peptide that is
FT cleaved to yield the mature functional enzyme"
FT 42..441
FT Protein
FT /label= mature_enzyme
FT 271..275
FT /note= "contains active site serine; conforms to
FT consensus motif for mammalian and microbial lipases and
FT serine proteases"
XX
XX
PN US5605801-A.
XX
XX 25-FEB-1997.
XX
XX 07-JUN-1995; 95US-00478465.
XX
XX 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray P, Tjoelker LW, Trong HL, Cousens LS, Wilder CL;
PI Eberhardt CD;
XX
XX WPI; 1997-153573/14.
DR N-PSDB; AAT63701.
DR
XX
XX Detection of platelet-activating factor acetyl:hydrolase gene mutation -
PT by restriction length polymorphism analysis.
PT
XX
XX Example 3; Col 33-38; 43pp; English.
PS
XX
XX This sequence is that of human platelet-activating factor acetyl-
CC hydrolase (PAF-AH). The claimed method of the invention detects a
CC mutation (which results in a V279F substitution) in the PAF-AH gene, and
CC comprises performing a restriction fragment length polymorphism analysis
CC and differentiating between wild-type and mutant alleles on the basis of
CC the number of restriction sites. The method is useful for diagnosis of
CC inherited PAF-AH deficiency, which has been correlated with severe
CC respiratory symptoms in asthmatic children. Recombinant PAF-AH can be
CC used to treat inflammatory conditions. (Updated on 25-MAR-2003 to correct
CC PF field.)
XX
SQ Sequence 441 AA;
Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 1.1e-217;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPPKLVHLCGCLAVVYFDWQYINPVAMKSSAWNKKIQVLMASFGQTKIPRGN 60
DB 1 MPPKLVHLCGCLAVVYFDWQYINPVAMKSSAWNKKIQVLMASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMFDHTNKGTFRLYYPQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
DB 61 GPYSVGCTDLMFDHTNKGTFRLYYPQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFLGSMTPPANWNSPLRPGSKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
DB 121 LRLFLGSMTPPANWNSPLRPGSKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSASATYFFKQSAAEIGDKSWLYLRTLKQBEETHIRNEQVRQRAKESQALSILIDID 240
DB 181 DRSASATYFFKQSAAEIGDKSWLYLRTLKQBEETHIRNEQVRQRAKESQALSILIDID 240
QY 241 HGKVPKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDRFCRGIADAWMF 300
DB 241 HGKVPKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDRFCRGIADAWMF 300
QY 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTFA 360
DB 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTFA 360

QY 361 TGKIIIGHMLKLGKGDIDSNAAIDLSNKAFLAPLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
DB 361 TGKIIIGHMLKLGKGDIDSNVAIDLSNKAFLAPLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
DB 421 NINTTNOHIMLQNSSGIEKYN 441
RESULT 7
AAW26498
ID AAW26498 standard; protein; 441 AA.
XX
XX AAW26498;
XX
XX 25-MAR-2003 (revised)
DT 05-JAN-1998 (first entry)
XX
XX Human platelet-activating factor acetylhydrolase.
DE
XX Platelet-activating factor acetylhydrolase; PAF-AH; human; inflammation;
KW asthma; pleurisy; necrotising enterocolitis;
KW adult respiratory distress syndrome; therapy.
XX
XX Homo sapiens.
OS
XX US5656431-A.
PN
XX 12-AUG-1997.
PD
XX 07-JUN-1995; 95US-00483232.
PF
XX 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
XX
XX (ICOS-) ICOS CORP.
PA
XX Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;
PI Eberhardt CD;
XX
XX WPI; 1997-414580/38.
DR N-PSDB; AAT87048.
DR
XX
XX Detecting lesions in human platelet-activating factor acetyl:hydrolase
PT gene - by comparison with defined wild-type gene sequence.
PT
XX Example 3; Col 47-50; 53pp; English.
PS
XX This polypeptide comprises human plasma platelet-activating factor
CC acetylhydrolase (PAF-AH), a protein that inactivates PAF and inactivates
CC oxidatively fragmented phospholipids such as products of the arachidonic
CC acid cascade that mediate inflammation. Its sequence was deduced from a
CC full-length cDNA clone (see AAT87048) obtained from a macrophage cDNA
CC library. Mouse, dog, cattle, chicken, rat and macaque PAF-AH polypeptides
CC (see AAW26500-505) have also been identified. Recombinant PAF-AH
CC polypeptides can be produced in prokaryotic or eukaryotic host cells and
CC used to mimic or augment normal processes of resolution of inflammation
CC in vivo. Examples describe the in vivo therapeutic effect of recombinant
CC PAF-AH products on acute inflammation, pleurisy, asthma, necrotising
CC enterocolitis and adult respiratory distress syndrome in animal models.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 441 AA;
Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 1.1e-217;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPPKLVHLCGCLAVVYFDWQYINPVAMKSSAWNKKIQVLMASFGQTKIPRGN 60
DB 1 MPPKLVHLCGCLAVVYFDWQYINPVAMKSSAWNKKIQVLMASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMFDHTNKGTFRLYYPQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Db 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFLGSMTPPANWNSPLRPGEKYLVPVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFLGSMTPPANWNSPLRPGEKYLVPVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSASATYYFKDQSAABEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILIDID 240
Db 181 DRSASATYYFKDQSAABEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILIDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQFRFCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQFRFCGIALDAWMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360
QY 361 TGKIIIGHMLKLKGDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQWDCLIEGDDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNVAIDLSNKASLAFLQKHLGLHKDFDQWDCLIEGDDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 8
AAW38361
ID AAW38361 standard; protein; 441 AA.
XX
AC AAW38361;
XX
DT 31-MAR-1998 (first entry)
XX
DE Human plasma platelet activating factor acetylhydrolase.
XX
KW Human; plasma platelet activating factor acetylhydrolase;
KW monoclonal antibody; immunoassay; diagnosis; asthma; detection.
XX
OS Homo sapiens.
XX
PN US5698403-A.
XX
PD 16-DEC-1997.
XX
PF 07-JUN-1995; 95US-00483140.
XX
PR 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;
PI Eberhardt CD;
XX
DR WPI; 1998-051484/05.
DR N-PSDB; AAT96127.
XX
PT Immunoassay for platelet activating factor acetylhydrolase, PAF-AH -
PT useful to diagnose disorders associated with abnormal PAF-AH level.
XX
PS Claim 1; Col 35-38; 47pp; English.
XX

CC The present sequence was used in the development of a method for
CC detecting human, mouse, canine, rat and monkey plasma platelet activating
CC factor acetylhydrolases (PAF-AH). The method comprises contacting serum
CC with PAF-AH specific monoclonal antibody (MAb) to form a PAF-AH/MAb
CC complex, and detecting the complex. The method can be used to diagnose
CC disorders associated with abnormal PAF-AH levels, and to monitor therapy
CC of such disorders. Plasma PAF-AH deficiency has been correlated with
CC severe respiratory symptoms in asthmatic children who appear to have

CC inherited the deficiency in an autosomal recessive manner
XX
SQ Sequence 441 AA;
Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 1.1e-217;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MVPPKLVHVLFCGCLAVVYFDFWQYINPVAHMKSSAWNKKIQVLMMAASFGQTKIPRGN 60
Db 1 MVPPKLVHVLFCGCLAVVYFDFWQYINPVAHMKSSAWNKKIQVLMMAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFLGSMTPPANWNSPLRPGEKYLVPVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFLGSMTPPANWNSPLRPGEKYLVPVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSASATYYFKDQSAABEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILIDID 240
Db 181 DRSASATYYFKDQSAABEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILIDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQFRFCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQFRFCGIALDAWMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360
QY 361 TGKIIIGHMLKLKGDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQWDCLIEGDDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNVAIDLSNKASLAFLQKHLGLHKDFDQWDCLIEGDDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 9
AAW96334
ID AAW96334 standard; protein; 441 AA.
XX
AC AAW96334;
XX
DT 28-JUN-1999 (first entry)
XX
DE Human plasma platelet-activating factor acetylhydrolase (PAF-AH).
XX
KW Plasma platelet activating factor acetylhydrolase; PAF-AH; PAF;
KW platelet activating factor; inflammation; treatment; hydrolysis;
KW augmentation; pleurisy; asthma; rhinitis; necrotizing enterocolitis;
KW acute respiratory distress syndrome; pancreatitis; neurological disease;
KW HIV; human immunodeficiency virus.
XX
OS Homo sapiens.
XX
PN WO9909147-A1.
XX
PD 25-FEB-1999.
XX
PF 13-AUG-1997; 97WO-US014212.
XX
PR 13-AUG-1997; 97WO-US014212.
XX
PA (ICOS-) ICOS CORP.
XX
PI Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
PI Wilder CL;
XX
DR WPI; 1999-181028/15.

DR N-PSDB; AAX08463.

XX New truncated human platelet-activating factor acetylhydrolase and its

PT encoding polynucleotides - useful for regulating inflammatory events.

XX

PS Claim 1; Page 97-98; 136pp; English.

XX

CC Plasma platelet-activating factor acetylhydrolase (PAF-AH) can be used to

CC inactivate the pathological effects of PAF. Pathological conditions which

CC can be treated include pleurisy, asthma, rhinitis, necrotizing

CC enterocolitis, acute respiratory distress syndrome, acute pancreatitis or

CC neurological disease associated with HIV infection. Identification and

CC isolation of polynucleotide sequences encoding human plasma PAF-AH allows

CC the recombinant production of PAF-AH. This makes possible the use of

CC exogenous PAF-AH to mimic or augment normal processes of resolution of

CC inflammation in vivo. PAF inactivation occurs by hydrolysis of the PAF sn

CC -2 acetyl group by PAF-AH. PAF-AH also metabolises oxidatively fragmented

CC phospholipids such as products of the arachidonic acid cascade which

CC mediate inflammation. Administration of PAF-AH is advantageous to

CC administering PAF receptor antagonists since PAF-AH is a product normally

CC found in plasma. Because PAF receptor antagonists are structurally

CC related to PAF they competitively inhibit native PAF-AH activity.

CC Treatment with recombinant PAF-AH would augment endogenous PAF-AH

CC activity and compensate for any inactivated endogenous enzyme

XX

SQ Sequence 441 AA;

Query Match 99.8%; Score 2354; DB 2; Length 441;

Best Local Similarity 99.8%; Pred. No. 1.1e-217;

Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPPKLHVLFCLCGCLAVVYFPDQYINPVAHMKSSAWNKIQVLMMAASFGQTKIPRGN 60

DB 1 MPPPKLHVLFCLCGCLAVVYFPDQYINPVAHMKSSAWNKIQVLMMAASFGQTKIPRGN 60

QY 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120

DB 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120

QY 121 LRLFFGSMTPANWNSPLRPEGEKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

DB 121 LRLFFGSMTPANWNSPLRPEGEKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

QY 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240

DB 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300

DB 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300

QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA 360

DB 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA 360

QY 361 TGKIIIGHMLKLGKGDIDSNVAIDLNSKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT 420

DB 361 TGKIIIGHMLKLGKGDIDSNVAIDLNSKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT 420

QY 421 NINTTNQHIMLQNSSGIEKYN 441

DB 421 NINTTNQHIMLQNSSGIEKYN 441

RESULT 10

AAW73359

ID AAW73359 standard; protein; 441 AA.

XX

AC AAW73359;

XX

DT 12-FEB-1999 (first entry)

XX

DE Human PAF-AH protein sequence.

XX Platelet-activating factor acetylhydrolase; PAF-AH; human; antibody.

XX Homo sapiens.

OS

PN US5847088-A.

XX

PD 08-DEC-1998.

XX

PF 07-JUN-1995; 95US-00485938.

XX

PR 06-OCT-1993; 93US-00133803.

PR 06-OCT-1994; 94US-00318905.

XX

PA (ICOS-) ICOS CORP.

XX

PI Wilder CL, Tjoelker LW, Gray P, Eberhardt CD, Cousens LS;

PI Trong HL;

XX

DR WPI; 1999-059148/05.

DR N-PSDB; AAV08534.

XX

PT Antibodies specific for platelet-activating factor acetylhydrolase

PT proteins - useful for detecting or purifying the proteins.

XX

PS Claim 1; Col 45-48; 59pp; English.

XX

CC This sequence represents the human platelet-activating factor

CC acetylhydrolase (PAF-AH). This protein is specifically bound by the

CC antibody of the invention. The monoclonal antibody of the invention is

CC useful for detecting or purifying PAF-AH proteins

XX

SQ Sequence 441 AA;

Query Match 99.8%; Score 2354; DB 2; Length 441;

Best Local Similarity 99.8%; Pred. No. 1.1e-217;

Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPPKLHVLFCLCGCLAVVYFPDQYINPVAHMKSSAWNKIQVLMMAASFGQTKIPRGN 60

DB 1 MPPPKLHVLFCLCGCLAVVYFPDQYINPVAHMKSSAWNKIQVLMMAASFGQTKIPRGN 60

QY 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120

DB 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120

QY 121 LRLFFGSMTPANWNSPLRPEGEKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

DB 121 LRLFFGSMTPANWNSPLRPEGEKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

QY 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240

DB 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300

DB 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300

QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA 360

DB 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA 360

QY 361 TGKIIIGHMLKLGKGDIDSNVAIDLNSKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT 420

DB 361 TGKIIIGHMLKLGKGDIDSNVAIDLNSKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT 420

QY 421 NINTTNQHIMLQNSSGIEKYN 441

DB 421 NINTTNQHIMLQNSSGIEKYN 441

RESULT 11

AAW88301

CC also have greater activity than the wild-type enzyme. This sequence
CC represents the human PAF-AH protein which is described in the method of
CC the invention
XX
SQ Sequence 441 AA;

Query Match 99.8%; Score 2354; DB 3; Length 441;
Best Local Similarity 99.8%; Pred. No. 1.1e-217;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPPKLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
Db 1 MPPPKLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60

QY 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120

QY 121 LRLFGSMTTPANWNSPLRPGKEYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTTPANWNSPLRPGKEYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

QY 181 DRSASATYYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDID 240
Db 181 DRSASATYYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDID 240

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRCGIALDAWMF 300

QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA 360

QY 361 TGKIIIGHMLKLKGDIDSNAAIDLSNKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNVAIDLSNKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT 420

QY 421 NINTTNQHIMLQNSSGIEKYN 441
Db 421 NINTTNQHIMLQNSSGIEKYN 441

RESULT 13
AAB07774
ID AAB07774 standard; protein; 441 AA.
AC AAB07774;
XX
DT 14-NOV-2000 (first entry)
XX Plasma platelet-activating factor acetylhydrolase.
XX Platelet-activating factor acetylhydrolase; platelet-activating factor;
KW reperfusion injury; acute inflammation; pleurisy; asthma;
KW necrotising enterocolitis; adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
PN US6099836-A.
XX
PD 08-AUG-2000.
XX
PF 19-JUN-1998; 98US-00100546.
XX
PR 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
PR 07-JUN-1995; 95US-00480658.
PR 22-JAN-1998; 98US-00010715.
XX
XX (ICOS-) ICOS CORP.
PA Eberhardt CD, Gray P, Trong HL, Tjoelker LW, Wilder CL;
XX
PI

PI Cousens LS;
XX
DR WPI; 2000-531654/48.
DR N-PSDB; AAA59579.
XX
PT Treating mammal susceptible to or suffering from platelet-activating
PT factor mediated condition associated with reperfusion injury such as
PT acute inflammation, pleurisy, asthma, necrotizing enterocolitis.
XX
PS Example 3; Col 49-52; 55pp; English.
XX
CC The specification describes a pharmaceutical composition comprising
CC platelet-activating factor acetylhydrolase. The composition is
CC administered for treating a mammal susceptible to or suffering from a
CC platelet-activating factor-mediated condition associated with reperfusion
CC injury. Diseases and conditions which may be treated include acute
CC inflammation, pleurisy, asthma, necrotising enterocolitis and adult
CC respiratory distress syndrome. The present sequence represents human
CC plasma platelet-activating factor acetylhydrolase
XX
SQ Sequence 441 AA;

Query Match 99.8%; Score 2354; DB 3; Length 441;
Best Local Similarity 99.8%; Pred. No. 1.1e-217;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPPPKLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
Db 1 MPPPKLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60

QY 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120

QY 121 LRLFGSMTTPANWNSPLRPGKEYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTTPANWNSPLRPGKEYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

QY 181 DRSASATYYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDID 240
Db 181 DRSASATYYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDID 240

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRCGIALDAWMF 300

QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA 360

QY 361 TGKIIIGHMLKLKGDIDSNAAIDLSNKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNVAIDLSNKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT 420

QY 421 NINTTNQHIMLQNSSGIEKYN 441
Db 421 NINTTNQHIMLQNSSGIEKYN 441

RESULT 14
AAE00761
ID AAE00761 standard; protein; 441 AA.
XX
AC AAE00761;
XX
DT 02-JUL-2001 (first entry)
XX
DE Human plasma platelet-activating factor acetylhydrolase (PAF-AH).
XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
KW antiinflammatory; septicemia; inflammation; haemostasis; parturition;
KW asthma; anaphylaxis; septic shock; antibacterial.
XX

```
OS XX Homo sapiens.
FH XX
FT XX Key Location/Qualifiers
FT XX Peptide 1..41
FT /note= "Hydrophobic segment containing 1-17 amino acids
FT of signal sequence plus an additional peptide that is
FT cleaved to yield the mature functional enzyme"
FT 42..441
FT Protein /label= Mature_human_PAF-AH_peptide
FT Domain /label= Consensus_motif
FT 271..275
FT
XX US6203790-B1.
XX 20-MAR-2001.
XX 23-MAY-2000; 2000US-00577758.
XX 06-OCT-1993; 93US-00133803.
XX 06-OCT-1994; 94US-00318905.
XX 07-JUN-1995; 95US-00480658.
XX 22-JAN-1998; 98US-00010715.
XX (ICOS-) ICOS CORP.
XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW,
XX Wilder CL;
XX WPI; 2001-280610/29.
XX N-PSDB; AAD04143.
XX
XX Treating a mammal susceptible to or suffering from septicemia comprises
XX administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
XX supplement endogenous PAF-AH activity and to inactivate pathological
XX amounts of PAF.
XX Claim 1; Col 47-50; 54pp; English.
XX
XX The present sequence is human plasma platelet-activating factor
XX acetylhydrolase (PAF-AH) protein. The invention relates to human plasma
XX platelet-activating factor acetylhydrolase (PAF-AH) and its corresponding
XX cDNA molecule. The invention also relates to method of treating a mammal
XX susceptible to or suffering from septicemia. PAF functions in normal
XX physiological processes such as inflammation, haemostasis and
XX parturition. PAF-AH specific antibodies are used in the diagnostic
XX methods to detect abnormal levels of PAF-AH in serum and also for
XX treating the pathological inflammatory conditions of PAF-AH such as
XX asthma, anaphylaxis, septic shock and arthritis. PAF-AH antibody is also
XX useful for screening a genetic lesion in the human plasma PAF-AH gene,
XX which occurs due to the replacement of nucleotide G to T at position 996
XX within exon 9 resulting in replacement of amino acid Val to Phe at
XX position 279. Thus the deficiency of PAF-AH activity is due to the
XX genetic lesion in human plasma PAF-AH gene
XX
XX Sequence 441 AA;
XX
XX Query Match 99.8%; Score 2354; DB 4; Length 441;
XX Best Local Similarity 99.8%; Pred. No. 1.1e-217;
XX Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 MVPKHLVFLCLCGCLAVVYFDFQYINPVAHMKSSAWNKKIQLVMAAASFGQTKIPRGN 60
Dd 1 MVPKHLVFLCLCGCLAVVYFDFQYINPVAHMKSSAWNKKIQLVMAAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Dd 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFLGSMTPPANWNSPLRPGEKYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Dd 121 LRLFLGSMTPPANWNSPLRPGEKYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240
```

```
Db 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFCGIALDAWMF 300
Dd 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFCGIALDAWMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
Dd 301 PLGDEVYSRIPQPLFFINSEYFQYPANIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
QY 361 TGKIIIGHMLKLKGDIDSNVAIDLNSKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Dd 361 TGKIIIGHMLKLKGDIDSNVAIDLNSKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Dd 421 NINTTNOHIMLQNSSGIEKYN 441
```

RESULT 15
AAB49451

ID AAB49451 standard; protein; 441 AA.

AC AAB49451;

DT 06-MAR-2001 (first entry)

DE Platelet-activating factor acetylhydrolase.

KW PAF-AH; antiallergic; antiinflammatory; platelet-activating factor;
KW PAF-acetylhydrolase; enzyme; pleurisy; asthma; rhinitis; human;
KW necrotizing enterocolitis; acute respiratory distress syndrome.

OS Homo sapiens.

PN US6146625-A.

PD 14-NOV-2000.

PF 22-JAN-1998; 98US-00010715.

PR 06-OCT-1993; 93US-00133803.

PR 06-OCT-1994; 94US-00318905.

PR 07-JUN-1995; 95US-00480658.

XX (ICOS-) ICOS CORP.

XX Gray P, Trong HL, Tjoelker LW, Wilder CL, Eberhardt CD;

XX Cousins LS;

XX WPI; 2001-040421/05.

XX N-PSDB; AAC89057.

XX Treating platelet-activating factor mediated pathologies such as asthma,

XX rhinitis, pleurisy and acute respiratory distress syndrome comprising

XX administering platelet-activating factor acetylhydrolase enzyme.

XX Claim 1; Col 47-50; 54pp; English.

XX The present invention relates to a method for treating a mammal

XX susceptible to or suffering from a platelet-activating factor (PAF)-

XX mediated pathological condition, comprising administering a composition

XX comprising PAF acetylhydrolase (PAF-AH) enzyme to supplement endogenous

XX PAF-AH activity and to inactivate pathological amounts of PAF in the

XX mammal. PAF-mediated pathological conditions are conditions such as

XX pleurisy, asthma, rhinitis, necrotizing enterocolitis and acute

XX respiratory distress syndrome in mammals. The present sequence is human

XX PAF-AH

XX Sequence 441 AA;

Query Match

99.8%; Score 2354; DB 4; Length 441;

Best Local Similarity 99.8%; Pred. No. 1.1e-217;		Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	MVPPKLVLCGCLAVVYPFDWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN	60
Db	1	MVPPKLVLCGCLAVVYPFDWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN	60
Qy	61	GPYVGCTDLMFDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI	120
Db	61	GPYVGCTDLMFDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI	120
Qy	121	LRLFGSMTPPANWNSPLRPGKYPVVFSGHGLGAFRTLISAIGIDLASHGFIVAAVEHR	180
Db	121	LRLFGSMTPPANWNSPLRPGKYPVVFSGHGLGAFRTLISAIGIDLASHGFIVAAVEHR	180
Qy	181	DRSASATYYPKQDSAAEIGDKSWLYLRTLQBEETHIRNEQVRQRAKESQALSILIDID	240
Db	181	DRSASATYYPKQDSAAEIGDKSWLYLRTLQBEETHIRNEQVRQRAKESQALSILIDID	240
Qy	241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF	300
Db	241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF	300
Qy	301	PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA	360
Db	301	PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFEA	360
Qy	361	TGKIIIGHMLKLGDDIDSNAADLSNKASLAFQKHLGKHDPDQWDCLIEGDDENLIPGT	420
Db	361	TGKIIIGHMLKLGDDIDSNAADLSNKASLAFQKHLGKHDPDQWDCLIEGDDENLIPGT	420
Qy	421	NINTTNOHIMLQNSSGIEKYN	441
Db	421	NINTTNOHIMLQNSSGIEKYN	441

Search completed: March 15, 2005, 10:03:43
Job time : 168.735 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 09:57:26 ; Search time 43.9559 Seconds
(without alignments)
748.938 Million cell updates/sec

Title: US-09-922-067F-14
Perfect score: 2358
Sequence: 1 MVPKLVHVLFCGCLAVV.....INTNQHIMQNSSGIEKYN 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2354	99.8	441	1 US-08-470-187-8	Sequence 8, Appli
2	2354	99.8	441	1 US-08-318-905-8	Sequence 8, Appli
3	2354	99.8	441	1 US-08-483-232-8	Sequence 8, Appli
4	2354	99.8	441	1 US-08-483-140-8	Sequence 8, Appli
5	2354	99.8	441	2 US-08-485-938A-8	Sequence 8, Appli
6	2354	99.8	441	2 US-08-910-041-8	Sequence 8, Appli
7	2354	99.8	441	3 US-09-328-474-8	Sequence 8, Appli
8	2354	99.8	441	3 US-09-100-546-8	Sequence 8, Appli
9	2354	99.8	441	3 US-09-010-715-8	Sequence 8, Appli
10	2354	99.8	441	3 US-09-577-758-8	Sequence 8, Appli
11	1964.5	83.3	444	2 US-08-485-938A-33	Sequence 33, Appl
12	1935.5	82.1	444	1 US-08-483-140-28	Sequence 28, Appl
13	1935.5	82.1	444	2 US-08-485-938A-32	Sequence 32, Appl
14	1514.5	64.2	440	1 US-08-483-140-27	Sequence 27, Appl
15	1514.5	64.2	440	2 US-08-485-938A-31	Sequence 31, Appl
16	1131.5	48.0	422	2 US-08-485-938A-34	Sequence 34, Appl
17	955	40.5	193	1 US-08-483-140-30	Sequence 30, Appl
18	955	40.5	193	2 US-08-485-938A-36	Sequence 36, Appl
19	797	33.8	392	2 US-08-886-152-3	Sequence 3, Appli
20	797	33.8	392	3 US-09-196-222-3	Sequence 3, Appli
21	747	31.7	392	2 US-08-886-152-1	Sequence 1, Appli
22	747	31.7	392	3 US-09-196-222-1	Sequence 1, Appli
23	672	28.5	171	1 US-08-483-140-29	Sequence 29, Appl
24	672	28.5	171	2 US-08-485-938A-35	Sequence 35, Appl
25	186	7.9	37	2 US-08-557-892-1	Sequence 1, Appli
26	186	7.9	37	2 US-08-387-858A-1	Sequence 1, Appli
27	186	7.9	37	3 US-09-294-384B-1	Sequence 1, Appli

28	186	7.9	37	3 US-08-717-079-1	Sequence 1, Appli
29	170	7.2	30	2 US-08-557-892-2	Sequence 2, Appli
30	170	7.2	30	2 US-08-387-858A-2	Sequence 2, Appli
31	170	7.2	30	3 US-09-294-384B-2	Sequence 2, Appli
32	170	7.2	30	3 US-08-717-079-2	Sequence 2, Appli
33	161.5	6.8	579	4 US-09-252-991A-32124	Sequence 32124, A
34	117.5	5.0	526	4 US-09-248-796A-19924	Sequence 19924, A
35	108	4.6	622	2 US-08-664-646A-2	Sequence 2, Appli
36	108	4.6	622	3 US-09-066-285-2	Sequence 2, Appli
37	108	4.6	622	3 US-09-261-006-2	Sequence 2, Appli
38	108	4.6	622	3 US-08-951-088-2	Sequence 2, Appli
39	108	4.6	622	4 US-09-609-566-2	Sequence 2, Appli
40	108	4.6	622	4 US-09-609-570-2	Sequence 2, Appli
41	108	4.6	622	4 US-09-427-372-2	Sequence 2, Appli
42	108	4.6	622	4 US-09-693-554-2	Sequence 2, Appli
43	106.5	4.5	275	4 US-09-198-452A-181	Sequence 181, App
44	106.5	4.5	287	4 US-09-438-185A-163	Sequence 163, App
45	104	4.4	20	2 US-08-557-892-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-470-187-8
; Sequence 8, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-470-187-8

Query Match 99.8%; Score 2354; DB 1; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;

Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MVPPKLVFLCCLAVVYFDDQYINPVVHMKSSAWVNKIQLVMAAASFGQTKIPRGN 60
Db 1 MVPPKLVFLCCLAVVYFDDQYINPVVHMKSSAWVNKIQLVMAAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMDFTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMDFTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Qy 121 LRLFGSMTTPANWNSPLRPEGEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTTPANWNSPLRPEGEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Qy 181 DRSASATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDID 240
Db 181 DRSASATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDID 240
Qy 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300
Qy 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIMKKCYSPDKERKMITIRGSHVQNFADFTFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIMKKCYSPDKERKMITIRGSHVQNFADFTFA 360
Qy 361 TGKIIIGHMLKLKGDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNVAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Qy 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 2

US-08-318-905-8
; Sequence 8, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-905-8

Query Match 99.8%; Score 2354; DB 1; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVPPKLVFLCCLAVVYFDDQYINPVVHMKSSAWVNKIQLVMAAASFGQTKIPRGN 60
Db 1 MVPPKLVFLCCLAVVYFDDQYINPVVHMKSSAWVNKIQLVMAAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMDFTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMDFTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Qy 121 LRLFGSMTTPANWNSPLRPEGEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTTPANWNSPLRPEGEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Qy 181 DRSASATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDID 240
Db 181 DRSASATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDID 240
Qy 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300
Qy 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIMKKCYSPDKERKMITIRGSHVQNFADFTFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIMKKCYSPDKERKMITIRGSHVQNFADFTFA 360
Qy 361 TGKIIIGHMLKLKGDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNVAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Qy 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 3

US-08-483-232-8
; Sequence 8, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-232-8

```

Query Match	99.8%;	Score 2354;	DB 1;	Length 441;
Best Local Similarity	99.8%;	Pred. No. 9.8e-246;		
Matches 440;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy 1	MVPPKHLVFLCIGCLAVVYPFDWQYINPVAHMKSSAWNKIQVLMAAASFGQTKIPRGN	60		
Dd 1	MVPPKHLVFLCIGCLAVVYPFDWQYINPVAHMKSSAWNKIQVLMAAASFGQTKIPRGN	60		
Qy 61	GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRDLDTLWIPNKKEYFWGLSKFLGTHWLMGNI	120		
Dd 61	GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRDLDTLWIPNKKEYFWGLSKFLGTHWLMGNI	120		
Qy 121	LRLLFSGMTTPANWNSPLRPGEKYPLVVFVSHGLGAFRTLYSAGIDILASHGEIVAAVEHR	180		
Dd 121	LRLLFSGMTTPANWNSPLRPGEKYPLVVFVSHGLGAFRTLYSAGIDILASHGEIVAAVEHR	180		
Qy 181	DRSASATYYFKDOSAAEIGDKSWLYLRTLKQBEETHIRNEQVRQRAKESQALSILDID	240		
Dd 181	DRSASATYYFKDOSAAEIGDKSWLYLRTLKQBEETHIRNEQVRQRAKESQALSILDID	240		
Qy 241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDQRFRCGIALDAWMF	300		
Dd 241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDQRFRCGIALDAWMF	300		
Qy 301	PLGDEVYSRIPOPLFFINSEYFOYPANIIKMKKCYSPPDKERKMITIRGSHVQNFADTFPA	360		
Dd 301	PLGDEVYSRIPOPLFFINSEYFOYPANIIKMKKCYSPPDKERKMITIRGSHVQNFADTFPA	360		
Qy 361	TGKIIIGHMLKLKGDIDSNAADLSNKAFLQKHLGLHKDPDQWDCLIEGDDENLIPGT	420		
Dd 361	TGKIIIGHMLKLKGDIDSNAADLSNKAFLQKHLGLHKDPDQWDCLIEGDDENLIPGT	420		
Qy 421	NINTTNOHIMLQNSSGIEKYN	441		
Dd 421	NINTTNOHIMLQNSSGIEKYN	441		

CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-140-8

Query Match	99.8%;	Score 2354;	DB 1;	Length 441;	
Best Local Similarity	99.8%;	Pred. No. 9.8e-246;			
Matches 440;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
QY	1	MVPPKHLVFLC	CGCLAVVYPFDWQYINPVAHMKSSAWVNKIQVLM	MAAASFGQTKIPRGN 60	
DB	1	MVPPKHLVFLC	CGCLAVVYPFDWQYINPVAHMKSSAWVNKIQVLM	MAAASFGQTKIPRGN 60	
QY	61	GPYSVGCTDLM	FDHTNKGTFRLRYPSQDNDRDLTLWIPNK	EYFWGLSKFLGTHWLMGNI 120	
DB	61	GPYSVGCTDLM	FDHTNKGTFRLRYPSQDNDRDLTLWIPNK	EYFWGLSKFLGTHWLMGNI 120	
QY	121	LRLLFGSMTTP	ANNNSPLRPGEKYPLVVF	SHGLGAFRTLYSAIGIDLASHGFIVA	VEHR 180
DB	121	LRLLFGSMTTP	ANNNSPLRPGEKYPLVVF	SHGLGAFRTLYSAIGIDLASHGFIVA	VEHR 180
QY	181	DRSASATYF	FKDQSAABIGDKSWLYLRTLKQEEETHIRNEQVR	QRAKECSQALSLLDID 240	
DB	181	DRSASATYF	FKDQSAABIGDKSWLYLRTLKQEEETHIRNEQVR	QRAKECSQALSLLDID 240	
QY	241	HGKPVKNALDL	KFDMEQKDSIDREKIAVIGHSGGATVIQTL	SEDRFCRGIALDAWMF 300	
DB	241	HGKPVKNALDL	KFDMEQKDSIDREKIAVIGHSGGATVIQTL	SEDRFCRGIALDAWMF 300	
QY	301	PLGDEVYSRI	PQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGS	VHQNFADFTFA 360	
DB	301	PLGDEVYSRI	PQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGS	VHQNFADFTFA 360	
QY	361	TGKIIGHMLKL	KGIDISNAADLSNKASLAFQKHLGLHKDPDQWDC	CLIEGDDENLIPGT 420	
DB	361	TGKIIGHMLKL	KGIDISNAADLSNKASLAFQKHLGLHKDPDQWDC	CLIEGDDENLIPGT 420	
QY	421	NINTTNQHIML	QNSSGIEKYN 441		
DB	421	NINTTNQHIML	QNSSGIEKYN 441		

RESULT 5
US-08-485-938A-8
; Sequence 8, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-8

Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 M V P P K L H V L F C L G C L A V V Y P F D W Q Y I N P V A H M K S S A W N K I Q V L M A A A S F G Q T K I P R G N 60
Db 1 M V P P K L H V L F C L G C L A V V Y P F D W Q Y I N P V A H M K S S A W N K I Q V L M A A A S F G Q T K I P R G N 60

Qy 61 G P Y S V G C T D L M F D H T N K G T F L R L Y Y P S Q D N R L D T L W I P N K E Y F W G L S K F L G T H W L M G N I 120
Db 61 G P Y S V G C T D L M F D H T N K G T F L R L Y Y P S Q D N R L D T L W I P N K E Y F W G L S K F L G T H W L M G N I 120

Qy 121 L R L L F G S M T T P A N W N S P L R P G E K Y P L V V F S H G L G A F R T L Y S A I G I D L A S H G F I V A A V E H R 180
Db 121 L R L L F G S M T T P A N W N S P L R P G E K Y P L V V F S H G L G A F R T L Y S A I G I D L A S H G F I V A A V E H R 180

Qy 181 D R S A S A T Y F K D Q S A A E I G D K S W L Y L R T L K Q E E T H I R N E Q V R Q R A K E C S Q A L S L I L D I D 240
Db 181 D R S A S A T Y F K D Q S A A E I G D K S W L Y L R T L K Q E E T H I R N E Q V R Q R A K E C S Q A L S L I L D I D 240

Qy 241 H G K P V K N A L D L K F D M E Q L K D S I D R E K I A V I G H S F G G A T V I Q T L S E D Q R F R C G I A L D A W M F 300
Db 241 H G K P V K N A L D L K F D M E Q L K D S I D R E K I A V I G H S F G G A T V I Q T L S E D Q R F R C G I A L D A W M F 300

Qy 301 P L G D E V Y S R I P O P L F F I N S E Y F O Y P A N I I K M K C Y S P D K E R K M I T I R G S V H Q N F A D F T F A 360
Db 301 P L G D E V Y S R I P O P L F F I N S E Y F O Y P A N I I K M K C Y S P D K E R K M I T I R G S V H Q N F A D F T F A 360

Qy 361 T G K I I G H M L K L K G D I D S N A A I D L S N K A S L A F L O K H L G L H K D F D Q W D C L I E G D D E N L I P G T 420
Db 361 T G K I I G H M L K L K G D I D S N A A I D L S N K A S L A F L O K H L G L H K D F D Q W D C L I E G D D E N L I P G T 420

Qy 421 N I N T T N Q H I M L O N S S G I E K Y N 441
Db 421 N I N T T N Q H I M L O N S S G I E K Y N 441

RESULT 6
US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-910-041-8

[illegible]

RESULT 7

US-09-328-474-8
; Sequence 8, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Heien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-328-474-8

Query Match 99.8%; Score 2354; DB 3; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 M V P P K L H V L F C L G C L A V V Y P F D W Q Y I N P V A H M K S S A W N K I Q V L M A A A S F G Q T K I P R G N 60
DB 1 M V P P K L H V L F C L G C L A V V Y P F D W Q Y I N P V A H M K S S A W N K I Q V L M A A A S F G Q T K I P R G N 60

QY 61 G P Y S V G C T D L M F D H T N K G T F L R L Y Y P S Q D N D R L D T L W I P N K E Y F W G L S K F L G T H W L M G N I 120
DB 61 G P Y S V G C T D L M F D H T N K G T F L R L Y Y P S Q D N D R L D T L W I P N K E Y F W G L S K F L G T H W L M G N I 120

QY 121 L R L L F G S M T T P A N W N S P L R P G E K Y P L V V F S H G L G A F R T L Y S A I G I D L A S H G F I V A A V E H R 180
DB 121 L R L L F G S M T T P A N W N S P L R P G E K Y P L V V F S H G L G A F R T L Y S A I G I D L A S H G F I V A A V E H R 180

QY 181 D R S A S A T Y Y F K D Q S A A E I G D K S W L Y L R T L K Q E E T H I R N E Q V R Q R A K E C S Q A L S L I L D I D 240
DB 181 D R S A S A T Y Y F K D Q S A A E I G D K S W L Y L R T L K Q E E T H I R N E Q V R Q R A K E C S Q A L S L I L D I D 240

QY 241 H G K P V K N A L D L K F D M E Q L K D S I D R E K I A V I G H S F G G A T V I Q T L S E D Q R F R C G I A L D A W M F 300
DB 241 H G K P V K N A L D L K F D M E Q L K D S I D R E K I A V I G H S F G G A T V I Q T L S E D Q R F R C G I A L D A W M F 300

QY 301 P L G D E V Y S R I P Q P L F F I N S E Y F Q Y P A N I I K M K K C Y S P D K E R K M I T I R G S V H Q N F A D F T P A 360
DB 301 P L G D E V Y S R I P Q P L F F I N S E Y F Q Y P A N I I K M K K C Y S P D K E R K M I T I R G S V H Q N F A D F T P A 360

QY 361 T G K I I G H M L K L K G D I D S N A A I D L S N K A S L A F L Q K H L G L H K D F D Q W D C L I E G D D E N L I P G T 420
DB 361 T G K I I G H M L K L K G D I D S N A A I D L S N K A S L A F L Q K H L G L H K D F D Q W D C L I E G D D E N L I P G T 420

QY 421 N I N T T N Q H I M L Q N S S G I E K Y N 441
DB 421 N I N T T N Q H I M L Q N S S G I E K Y N 441

RESULT 8
US-09-100-546-8
; Sequence 8, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

```

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/09/100,546
CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: US/09/010,715
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6099836and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-100-546-8

Query Match 99.8%; Score 2354; DB 3; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MVPPKLVLFCLCGCLAVVYPPDQYINPVAHMKSSAWNKKIQVLMAAASFGQTKIPRGN 60
Db 1 MVPPKLVLFCLCGCLAVVYPPDQYINPVAHMKSSAWNKKIQVLMAAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMFDHTNKGTFRLRYPSQDNRDLTLWI PNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDHTNKGTFRLRYPSQDNRDLTLWI PNKEYFWGLSKFLGTHWLMGNI 120
Qy 121 LRLFGSMTTPANWNSPLRPGEKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTTPANWNSPLRPGEKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Qy 181 DRASATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILID 240
Db 181 DRASATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILID 240
Qy 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSPGGATVIQTLSEDRFCGIALDAMWF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSPGGATVIQTLSEDRFCGIALDAMWF 300
Qy 301 PLGDEVYSRIPQPLFFINSEYFQY PANI IKMKKCYSPDKERKMITIRGSHVQNFAFTFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQY PANI IKMKKCYSPDKERKMITIRGSHVQNFAFTFA 360
Qy 361 TGKIIIGHMLKLKGDIDSNAIDLNSKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNAIDLNSKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Qy 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 9
US-09-010-715-8
Sequence 8, Application US/09010715
Patent No. 6146625
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6146625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-010-715-8

Query Match 99.8%; Score 2354; DB 3; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MVPPKLVLFCLCGCLAVVYPPDQYINPVAHMKSSAWNKKIQVLMAAASFGQTKIPRGN 60
Db 1 MVPPKLVLFCLCGCLAVVYPPDQYINPVAHMKSSAWNKKIQVLMAAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMFDHTNKGTFRLRYPSQDNRDLTLWI PNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDHTNKGTFRLRYPSQDNRDLTLWI PNKEYFWGLSKFLGTHWLMGNI 120
Qy 121 LRLFGSMTTPANWNSPLRPGEKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTTPANWNSPLRPGEKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Qy 181 DRASATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILID 240
Db 181 DRASATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILID 240

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQTLSEDOFRFCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQTLSEDOFRFCGIALDAWMF 300
QY 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFPA 360
Db 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFPA 360
QY 361 TGKIIIGHMLKLKGDIDSNAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 10
US-09-577-758-8
; Sequence 8, Application US/09577758
; Patent No. 6203790
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,758
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/010,715
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6203790and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-577-758-8

Query Match 99.8%; Score 2354; DB 3; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVPPKLHVLFCGCLAVVYFPDQYINPVAHMKSSAWNKIQVLMMAASFGQTKIPRGN 60
Db 1 MVPPKLHVLFCGCLAVVYFPDQYINPVAHMKSSAWNKIQVLMMAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFGSMTTPANWNSPLRPEGEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180
Db 121 LRLFGSMTTPANWNSPLRPEGEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180
QY 181 DRSASATYFPKQDQSAABEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSLLDID 240
Db 181 DRSASATYFPKQDQSAABEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSLLDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQTLSEDOFRFCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQTLSEDOFRFCGIALDAWMF 300
QY 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFPA 360
Db 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFPA 360
QY 361 TGKIIIGHMLKLKGDIDSNAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 11
US-08-485-938A-33
; Sequence 33, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-938A-33

Query Match 83.3%; Score 1964.5; DB 2; Length 444;
Best Local Similarity 82.4%; Pred. No. 1.4e-203;
Matches 364; Conservative 39; Mismatches 38; Indels 1; Gaps 1;

Qy 1 MVPPKLVLCGCLAVVYFDFWQYINPVVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60
Db 1 MLPSKLVLCGCLAVVYFDFWQYINPVVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Qy 121 LRLFGSMTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Qy 181 DRASATYFVKDQSAAEIGDKSWLYLRTLKQ-EEETHIRNEQVRORAKESQALSILDI 239
Db 181 DGSASSTYFVKDQSAEIGDKSWLYLRTLKRGEEFFPLRNEQLRORAKESQALSILDI 240
Qy 240 DHGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDQRCGIALDAWM 299
Db 241 DHGRPVTVNLDLEFVQQLKDSIDRDKIAIGHSGFGATVIQTLSEDQRCGIALDAWM 300
Qy 300 FPLGDEVYSRIPQPLFFINSEYFQYPANIKMKKCYSPDKERKMITIRGSHQNFADFTF 359
Db 301 FPLGDEVYSRIPQPLFFINSEYFQYPANIKMKKCYSPDKERKMITIRGSHQNFADFTF 360
Qy 360 ATGKIIGHMLKLKGDIDSNAAIDLSNKAFLQKHLGLHDKDFDQWDCLEGGDENLIPG 419
Db 361 ATSKIIGYFTLKGIDSNVAISLSNKAFLQKHLGLQKDFDQWDSLVEGEDHNLIPG 420
Qy 420 TNINTNQHIMLQNSSGIEKYN 441
Db 421 TNINTNQHAILQNSTGIERN 442

RESULT 12
US-08-483-140-28
Sequence 28, Application US/08483140
Patent No. 5698403
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-140-28

Query Match 82.1%; Score 1935.5; DB 1; Length 444;
Best Local Similarity 80.8%; Pred. No. 2e-200;
Matches 357; Conservative 38; Mismatches 46; Indels 1; Gaps 1;

Qy 1 MVPPKLVLCGCLAVVYFDFWQYINPVVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60
Db 1 MLPPKLVLCGCLAVVYFDFWQYINPVVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Qy 121 LRLFGSMTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Qy 181 DRASATYFVKDQSAAEIGDKSWLYLRTLKQ-EEETHIRNEQVRORAKESQALSILDI 239
Db 181 DGSASATYFVKDQSAAEIGDKSWLYLRTLKQ-EEETHIRNEQVRORAKESQALSILDI 240
Qy 240 DHGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDQRCGIALDAWM 299
Db 241 DHGRPVTVNLDLEFVQQLKDSIDRDKIAIGHSGFGATVIQTLSEDQRCGIALDAWM 300
Qy 300 FPLGDEVYSRIPQPLFFINSEYFQYPANIKMKKCYSPDKERKMITIRGSHQNFADFTF 359
Db 301 LPLDDAIYSRIPQPLFFINSEYFQYPANIKMKKCYSPDKERKMITIRGSHQNFADFTF 360
Qy 360 ATGKIIGHMLKLKGDIDSNAAIDLSNKAFLQKHLGLHDKDFDQWDCLEGGDENLIPG 419
Db 361 TTGKIIVGYFTLKGIDSNVAIDLSNKAFLQKHLGLRDKDFDQWDSLIEGKDNLMFG 420
Qy 420 TNINTNQHIMLQNSSGIEKYN 441
Db 421 TNINTNEHDTLQNSPEAKSN 442

RESULT 13
US-08-485-938A-32
Sequence 32, Application US/08485938A
Patent No. 5847088
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5847088and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32792
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-938A-32

Query Match 82.1%; Score 1935.5; DB 2; Length 444;
Best Local Similarity 80.8%; Pred. No. 2e-200;
Matches 357; Conservative 38; Mismatches 46; Indels 1; Gaps 1;
QY 1 MPPKLVLCGCLAVVYDFDQYINPVVHMKSSAWNKIQVLMASAFGQTKIPRGN 60
Db 1 MLPPKLHALFCLCSCLTLVHPIDWQDLNPVVAHRSASAWANKIQALMAASIRQSRIPKGN 60
QY 61 GPYSVGCTDLMPDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GSYSVGCTDLMPDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGKI 120
QY 121 LRLFGSMTTPANWNSPLRPGCEKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LSFFFGSVTTTPANWNSPLRPGCEKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAIEHR 180
QY 181 DRSASATYYPKQDSAAEIGDKSWLYLRTLKQ-EEETHIRNEQVRQRAKESQALSILDI 239
Db 181 DGSASATYYPKQDSAAEIGDKSWLYLRTLKQ-EEETHIRNEQVRQRAKESQALNLI 240
QY 240 DHGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVITQTLSEDQRFRCGIALDAMW 299
Db 241 DHGRPIKNVLDFEVDQELKDSIDRDKIAVIGHSGFGGATVITQTLSEDQRFRCGIALDAMW 300
QY 300 FPLGDEVYSRIPQLFFINSEYFQYPANI IKMKKCYSPDKERKMITIRGSHQNFADFTF 359
Db 301 LPLDDAIYSRIPQLFFINSEYFQYPENI IKMKKCYSPDKERKMITIRGSHQNFADFTF 360
QY 360 ATGKIIGHMLKLKGDIDSNAAIDLSNKAFLQKHLGLHDFDQWDCLEGGDLENLIPG 419
Db 361 TTGKIVGYIFTLKGDIDSNVAIDLCKNKAFLQKHLGLHDFDQWDCLEGGDLENLIPG 420
QY 420 TNINTTNOHIMLQNSSGIEKYN 441

Db 421 TNINITNEHDTLQNSPEAKSN 442
RESULT 14
US-08-483-140-27
Sequence 27, Application US/08483140
Patent No. 5698403
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 440 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-140-27
Query Match 64.2%; Score 1514.5; DB 1; Length 440;
Best Local Similarity 65.8%; Pred. No. 7.4e-155;
Matches 290; Conservative 55; Mismatches 95; Indels 1; Gaps 1;
QY 1 MPPKLVLCGCLAVVYDFDQYINPVVHMKSSAWNKIQVLMASAFGQTKIPRGN 60
Db 1 MVPLKLQALFCLLCLLPVHPFHWDTSF-DPRPSVMFHLQSVMSAAGSGHSKIPKGN 59
QY 61 GPYSVGCTDLMPDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 60 GSYSVGCTDLMPFGYGNESVRLYYPAQDQGRDLTVWIPNKEYFLGLSIFLGTSPVIGNI 119
QY 121 LRLFGSMTTPANWNSPLRPGCEKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 120 LHLLYGSLTTPASWNSPLRPGCEKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVATVEHR 179
QY 181 DRSASATYYPKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDI 240
Db 180 DRSASATYYPKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDI 239
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVITQTLSEDQRFRCGIALDAMWF 300
Db 240 HGDPKENVLGSAFDMKQLKDAIDETKIALMGHSGFGGATVITQTLSEDQRFRCGVALDPWMY 299

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 10:07:52 ; Search time 131.868 Seconds
(without alignments)
1103.088 Million cell updates/sec

Title: US-09-922-067F-14
Perfect score: 2358
Sequence: 1 MVPKLVLCGCLAVVY.....INTTQHIMLQNSGIEKYN 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2358	100.0	441	16	US-10-741-601-373	Sequence 373, App
2	2358	100.0	441	16	US-10-741-601-374	Sequence 374, App
3	2354	99.8	441	9	US-09-729-402-8	Sequence 8, Appli
4	2354	99.8	441	14	US-10-003-978A-8	Sequence 8, Appli
5	2354	99.8	441	14	US-10-161-127-1	Sequence 1, Appli
6	2354	99.8	441	16	US-10-755-889-278	Sequence 278, App
7	797	33.8	392	10	US-09-961-253-3	Sequence 3, Appli
8	747	31.7	392	10	US-09-961-253-1	Sequence 1, Appli
9	497	21.1	384	15	US-10-369-493-5034	Sequence 5034, Ap
10	493.5	20.9	476	15	US-10-369-493-6760	Sequence 6760, Ap
11	295.5	12.5	438	15	US-10-369-493-2350	Sequence 2350, Ap
12	205	8.7	439	15	US-10-354-437-112	Sequence 112, App
13	202	8.6	401	14	US-10-156-761-8015	Sequence 8015, Ap

14	186	7.9	37	9	US-09-922-067-1	Sequence 1, Appli
15	186	7.9	37	14	US-10-173-233-1	Sequence 1, Appli
16	186	7.9	37	14	US-10-406-156-1	Sequence 1, Appli
17	170	7.2	30	9	US-09-922-067-2	Sequence 2, Appli
18	170	7.2	30	14	US-10-173-233-2	Sequence 2, Appli
19	170	7.2	30	14	US-10-406-156-2	Sequence 2, Appli
20	163	6.9	407	14	US-10-156-761-8357	Sequence 8357, Ap
21	122.5	5.2	273	15	US-10-369-493-11644	Sequence 11644, A
22	122.5	5.2	273	15	US-10-369-493-15162	Sequence 15162, A
23	122.5	5.2	275	15	US-10-369-493-14679	Sequence 14679, A
24	115	4.9	352	14	US-10-102-239-5	Sequence 5, Appli
25	114.5	4.9	262	14	US-10-102-239-7	Sequence 7, Appli
26	114.5	4.9	315	15	US-10-424-599-188557	Sequence 188557, A
27	111	4.7	301	14	US-10-102-239-4	Sequence 4, Appli
28	110.5	4.7	262	14	US-10-102-239-6	Sequence 6, Appli
29	110.5	4.7	739	15	US-10-282-122A-53623	Sequence 53623, A
30	108	4.6	622	9	US-09-966-803-2	Sequence 2, Appli
31	106.5	4.5	275	15	US-10-289-762-181	Sequence 181, App
32	104.5	4.4	868	15	US-10-282-122A-77289	Sequence 77289, A
33	104	4.4	20	9	US-09-922-067-11	Sequence 11, Appli
34	104	4.4	20	14	US-10-173-233-11	Sequence 11, Appli
35	104	4.4	20	14	US-10-406-156-11	Sequence 11, Appli
36	104	4.4	27	9	US-09-922-067-3	Sequence 3, Appli
37	104	4.4	27	14	US-10-173-233-3	Sequence 3, Appli
38	104	4.4	27	14	US-10-406-156-3	Sequence 3, Appli
39	103.5	4.4	473	15	US-10-369-493-13571	Sequence 13571, A
40	103.5	4.4	931	15	US-10-369-493-22397	Sequence 22397, A
41	103.5	4.4	931	16	US-10-723-807-11	Sequence 11, Appli
42	103.5	4.4	1153	16	US-10-437-963-140880	Sequence 140880, A
43	103	4.4	790	15	US-10-369-493-3803	Sequence 3803, Ap
44	102	4.3	330	15	US-10-425-114-36813	Sequence 36813, A
45	102	4.3	684	15	US-10-425-114-57854	Sequence 57854, A

ALIGNMENTS

RESULT 1
US-10-741-601-373
; Sequence 373, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-373

Query Match	100.0%	Score	2358	DB	16	Length	441
Best Local Similarity	100.0%	Pred. No.	1.5e-226	Mismatches	0	Indels	0
Matches	441	Conservative	0	Mismatches	0	Gaps	0
QY	1	MVPPKLVLCGCLAVVYFDWQYINPVAHMKSSAWNKIQVLMMAASFGOTKIPRGN	60				
Db	1	MVPPKLVLCGCLAVVYFDWQYINPVAHMKSSAWNKIQVLMMAASFGOTKIPRGN	60				
QY	61	GPYSVGCTDLMFDHTNKGTFRLYYPQNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI	120				
Db	61	GPYSVGCTDLMFDHTNKGTFRLYYPQNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI	120				
QY	121	LRLFLGSMITPANWNSPLRPEKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180				
Db	121	LRLFLGSMITPANWNSPLRPEKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180				
QY	181	DRSASATYFKDQSAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKCSQALSILIDID	240				

Db 181 DRSATYFQDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSFGGATVIQTLSEDQRFRCGIALDAMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSFGGATVIQTLSEDQRFRCGIALDAMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
QY 361 TGKIIIGHMLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 2
US-10-741-601-374
; Sequence 374, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-374

Query Match 100.0%; Score 2358; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.5e-226;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVPPKLVFLCLCGCLAVVYFDFWQYINPVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60
Db 1 MVPPKLVFLCLCGCLAVVYFDFWQYINPVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMFDHTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDHTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLLFSGMTTPANWNSPLRPGEKYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLLFSGMTTPANWNSPLRPGEKYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSATYFQDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240
Db 181 DRSATYFQDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSFGGATVIQTLSEDQRFRCGIALDAMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSFGGATVIQTLSEDQRFRCGIALDAMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
QY 361 TGKIIIGHMLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441

Db 421 NINTTNOHIMLQNSSGIEKYN 441
RESULT 3
US-09-729-402-8
; Sequence 8, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,402
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20010021379Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-729-402-8

Query Match 99.8%; Score 2354; DB 9; Length 441;
Best Local Similarity 99.8%; Pred. No. 3.9e-226;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVPPKLVFLCLCGCLAVVYFDFWQYINPVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60
Db 1 MVPPKLVFLCLCGCLAVVYFDFWQYINPVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMFDHTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDHTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLLFSGMTTPANWNSPLRPGEKYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLLFSGMTTPANWNSPLRPGEKYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSATYFQDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDID 240

Db 181 DRSATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRFCIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRFCIALDAWMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFFA 360
QY 361 TGKIIIGHMLKLGKGDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLGKGDIDSNVAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 4
US-10-003-978A-8
; Sequence 8, Application US/10003978A
; Publication No. US20030072747A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, Gerstein & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6357
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/003,978A
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/729,402
; FILING DATE: 04-DEC-2000
; APPLICATION NUMBER: US 09/577,758
; FILING DATE: 23-MAY-2000
; APPLICATION NUMBER: US 09/010,715
; FILING DATE: 22-JAN-1998
; APPLICATION NUMBER: US 08/480,658
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030072747Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/37792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-003-978A-8
Query Match 99.8%; Score 2354; DB 14; Length 441;
Best Local Similarity 99.8%; Pred. No. 3.9e-226;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPPPKLHVLFCGCLAVVYFEDWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
Db 1 MPPPKLHVLFCGCLAVVYFEDWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFGSMTTPANWNSPLRPGEKYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTTPANWNSPLRPGEKYPLVVFSGHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240
Db 181 DRSATYFVKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240
QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRFCIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRFCIALDAWMF 300
QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFFA 360
QY 361 TGKIIIGHMLKLGKGDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLGKGDIDSNVAIDLSNKASLAFLQKHLGLHKDFDQWDCLEGGDENLIPGT 420
QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 5
US-10-161-127-1
; Sequence 1, Application US/10161127
; Publication No. US20030166225A1
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; TITLE OF INVENTION: ISOLATED GENOMIC POLYNUCLEOTIDE FRAGMENTS THAT ENCODE
; LIPOPROTEIN-ASSOCIATED PHOSPHOLIPASE A2
; FILE REFERENCE: JR-16,001
; CURRENT APPLICATION NUMBER: US/10/161,127
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/294,404
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-127-1

Query Match 99.8%; Score 2354; DB 14; Length 441;
Best Local Similarity 99.8%; Pred. No. 3.9e-226;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MPPPKLHVLFCGCLAVVYFEDWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
Db 1 MPPPKLHVLFCGCLAVVYFEDWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMFDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Db 61 GPYSGVCTDLMFDHTNKGTFURLYYPSQDNDRLDRTLWIPNKEYFWGLSKFLGTHWLMGNI 120

QY 121 LRLFLGSMTPANWNSPLRPGCKEYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

Db 121 LRLFLGSMTPANWNSPLRPGCKEYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

QY 181 DRSASATYYPKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240

Db 181 DRSASATYYPKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300

Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300

QY 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360

Db 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360

QY 361 TGKIIIGHMLKLGDISNAAIDLSNKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420

Db 361 TGKIIIGHMLKLGDISNVAIDLSNKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420

QY 421 NINTTNOHIMLQNSSGIEKYN 441

Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 6

US-10-755-889-278

; Sequence 278, Application US/10755889

; Publication No. US20040171823A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB

; FILE REFERENCE: D0284 NP

; CURRENT APPLICATION NUMBER: US/10/755,889

; CURRENT FILING DATE: 2004-01-13

; PRIOR APPLICATION NUMBER: U.S. 60/440,068

; PRIOR FILING DATE: 2003-01-14

; PRIOR APPLICATION NUMBER: U.S. 60/469,757

; PRIOR FILING DATE: 2003-05-12

; NUMBER OF SEQ ID NOS: 823

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 278

; LENGTH: 441

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-755-889-278

Query Match 99.8%; Score 2354; DB 16; Length 441;

Best Local Similarity 99.8%; Pred. No. 3.9e-226;

Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVPKHLVFLCLCGCLAVVYPPDQYINPVAHMKSSAWYKIQVLMAAASFGQTKIPRGN 60

Db 1 MVPKHLVFLCLCGCLAVVYPPDQYINPVAHMKSSAWYKIQVLMAAASFGQTKIPRGN 60

QY 61 GPYSGVCTDLMFDHTNKGTFURLYYPSQDNDRLDRTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Db 61 GPYSGVCTDLMFDHTNKGTFURLYYPSQDNDRLDRTLWIPNKEYFWGLSKFLGTHWLMGNI 120

QY 121 LRLFLGSMTPANWNSPLRPGCKEYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

Db 121 LRLFLGSMTPANWNSPLRPGCKEYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

QY 181 DRSASATYYPKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240

Db 181 DRSASATYYPKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300

Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQRFRCGIALDAWMF 300

QY 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360

Db 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360

QY 361 TGKIIIGHMLKLGDISNAAIDLSNKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420

Db 361 TGKIIIGHMLKLGDISNVAIDLSNKASLAFQKHLGLHKDFDQWDCLEGGDENLIPGT 420

QY 421 NINTTNOHIMLQNSSGIEKYN 441

Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 7

US-09-961-253-3

; Sequence 3, Application US/09961253

; Publication No. US20030040093A1

; GENERAL INFORMATION:

; APPLICANT: ADACHI, HIDEKI

; TSUJIMOTO, MASAFUMI

; ARAI, HIROYUKI

; INOUE, KEIZO

; TITLE OF INVENTION: PLATELET ACTIVATING FACTOR

; ACETYLHYDROLASE, AND GENE THEREOF

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/961,253

; FILING DATE: 25-Sep-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/196,222

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/886,152

; FILING DATE: 30-JUN-1997

; APPLICATION NUMBER: JP 8-188369

; FILING DATE: 28-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 2292-041-0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 392 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; ORIGINAL SOURCE:

; ORGANISM: HUMAN

; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-961-253-3

Query Match 33.8%; Score 797; DB 10; Length 392;

Best Local Similarity 43.5%; Pred. No. 1.6e-70;

Matches 163; Conservative 71; Mismatches 129; Indels 12; Gaps 6;

Db	14	KMP---	GQFKVGCMDLMIEEAAGSGLFMRLLFFPT-DSEITGPSSLPVWIPRPEYAYGVGE	69
QY	110	FLG-THWLMGNILRL	LLFGSMITTPANWNSPL-RPGEKYPVLVFSHGLGAFRTLYSAIGIDL	167
Db	70	YLGHSPHQMDLISS	LVIGDKRVDICDNAQLSTKSDKPWVLVFSHGLGGSRTFYSTYCTSL	129
QY	168	ASHGEIVAAVEHRDRS	ASATYFYFKDQSAABEIGDKSWLYLRTLKQEETHIRNEQVQRQAK	227
Db	130	ASHGYVVAAVEHRDSS	ACWTYKLVKNGTGLVEKPKMIKLAVDRNDKQFKIRNEQVGKRAE	189
QY	228	ECSQALSILIDIDH	GKPVKNALDL--KFDMEQLKDSIDREKIAVIGHSGFGGATVIQTISE	285
Db	190	ECAKAVKILEQLDS	GN-VKDKVIGNNANLEFFKNKLLTTTASIIIGHSGFGGATSIASSSS	248
QY	286	DORFRCGIALDAWN	PPLGDEVYSRIPOPLFFINSEYFQYPANIIMKKKCYSPDKERKMIT	345
Db	249	D--FQKAI	VLGDGWNYPDLQDNQQEQAKQPIMFLNVGDQWQNNENLEVMRKILPNNEGNILLT	306
QY	346	IRGSVHQNFADFT	FATGKIIGHMLKLKGDIDSNAAIDLSNKASLAFIQ	393
Db	307	LGSVAVHQSF	TDFPFPVFNWLAKQFVGHGPTPEYLCMQSAIELTSLFK	354

RESULT 10
 US-10-369-493-6760
 ; Sequence 6760, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 6760
 ; LENGTH: 476
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 US-10-369-493-6760

```

Db      364 KQPTLFNVGDWQWENLDVMKKIISHNDGNLALTNGAVHQCFSDFPFIFPSWLAKKFG 423
QY      371 LKGDIDSNAIDLSNKASLAFIQ 393
Db      424 VQGRTEPSLCMQAAIELSLAFLE 446

RESULT 11
US-10-369-493-2350
; Sequence 2350, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2350
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2350

```

RESULT 12
US-10-354-437-112
; Sequence 112, Application US/10354437
; Publication No. US20040023257A1

; GENERAL INFORMATION:
; APPLICANT: Barton, Nelson R.
; APPLICANT: Weiner, David Paul
; APPLICANT: Greenberg, William
; APPLICANT: Luu, Samantha
; APPLICANT: Chang, Kristine
; APPLICANT: Waters, Elizabeth
; TITLE OF INVENTION: ENZYMES HAVING SECONDARY AMIDASES ACTIVITY
; FILE REFERENCE: 09010-106001
; CURRENT APPLICATION NUMBER: US/10/354,437
; CURRENT FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: US 60/352,895
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
US-10-354-437-112

Query Match 8.7%; Score 205; DB 15; Length 439;
Best Local Similarity 23.4%; Pred. No. 3.1e-11;
Matches 101; Conservative 59; Mismatches 127; Indels 144; Gaps 21;
QY 61 GYSVGTDLMPDHTNKGTFRLYPSQDNDRLD-----TLWIPNKEYFWGLSKFLGT- 113
Db 77 GTYKVGTTTLMLEDK-----RREEPATE-DRADRRRLMIQIWPAAE-----AGTG 120
QY 114 -----HWLMGNILRLFLGSMTPPANWNSPI-----RPGKYPLVVFVSH 151
Db 121 SGKAPYIEH--LPVLEGLRQISMPFFLLSQLKYQVPYAMQDAEVSRRDQERYPVLLFSH 178
QY 152 GLGAFRTLYSAIGIDLASHGFVAAVEHRDRSASATYYPKDOSA-AEIG-----DK 201
Db 179 GLSGFRNQNTFQVTELASRGYIVVGIDHAYDAAAV--FPDRTAMLKGLNLSGFDAYEEK 236
QY 202 SWLYRLTKQBEETHIRNEQVQRACECSQALSILIDIDHGKPVKNALDLKFDMEQLKDS 261
Db 237 SRLWV-----EDAKFVLDELRMSGPAASGFLSGRLDMD----- 270
QY 262 IDREKIAVIGHSGGATVIQTLSEDQFRFCGIALDAWMP--PLGDEVYSRIPQLFFINS 319
Db 271 ----KIGMFGHSGGATAAQMLLADSRVKAALNMDGTLYGQVPPEGFGK---PYMQMNA 323
QY 320 E-----YFQYPANIIKMKKCYSPDKERKMITIRGSHVQNF 354
Db 324 ELSIDRAVFEQSLDRAMASSGRSREDEYQFWAESVE-RRSRAESGEAHTIIPAHANHMSF 382
QY 355 ADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLAFLQHLGLHKDFDQWDCLEGGDDE 414
Db 383 TDF-----YLFSPLLPPKG-ABPRQMHSINALSAAF-----FDQY---VKGD-- 421
QY 415 NLIRPTNINTT 425
Db 422 ---PGASVEKT 429

RESULT 13
US-10-156-761-8015
; Sequence 8015, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8015
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8015
Query Match 8.6%; Score 202; DB 14; Length 401;
Best Local Similarity 23.9%; Pred. No. 5.3e-11;
Matches 96; Conservative 67; Mismatches 157; Indels 82; Gaps 21;
QY 29 PVAHMKSSAWVNKIQVLMAAASFGQTKIPRGNGPYSVGCTDLMF-----DHTNKGTF 81
Db 26 PLAAVAGPAWADP-----AAPAVTRLMLPVTGPHPGVGTQVLHLVDRSRPDDIAGPGHER 80
QY 82 RL-----YYPQDNDRDLTL-WIPNKEYFWGLSKFLGTHLWLMGNILRLFLGSMTPPANWNS 136
Db 81 ELMATVWPARDVQRYPVAPWMP-----AGALQAFLADAGFSA-LVRL--GPLTA-GHVG 132
QY 137 PL-RPGEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHRDRSASATYYPKDOSA 195
Db 133 PVRRSGRRLPVVVFVSHGAHSHQGDHTVMVQELASHGYAAVTVAH--QYDTYTFPDGRIA 190
QY 196 AEIGDKSWLYRLTKQBEETHIR--NEQVQRACECSQALSILIDIDHGKPVKNALDLKF 253
Db 191 VPLHDGQ---APTLPGDFAADLRFVLDCEVLAAGCNP-----DVDHRELPAGLL---- 237
QY 254 DMEQLKDSIDREKIAVIGHSGFGG-ATVIQTLSEDQFRFCGIALDAWMPPLGDEVYSRIPQ 312
Db 238 -----GSLDPRRVGAFGWSKGGTATACATLA-DERIRAGLSLDGPM-QMNPPLAGDLDR 289
QY 313 PLFFINSEYFQYPANIIKMKKCYSPDKE-----RKMITIRGSHVQNFAD---FT 358
Db 290 PFMMSAVTR-----ATDPEAAAFWSHLRGWRLNIQAQGAHVSVYGDNEALF 337
QY 359 FATGKIIG-----HMLKLKGDIDSNAAIDLSNKASLAFLQKHL 396
Db 338 PQVAKLWGSQQQLQDVIGTLDPPDQAVKIQQAYPLAFFDEHL 379

RESULT 14
US-09-922-067-1
; Sequence 1, Application US/09922067
; Patent No. US20020177209A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
; TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
; Thereof And Use Of The Same In Diagnosis And Therapy
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,067
FILING DATE: 03-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/193,130
FILING DATE: 1998-11-17
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
FEATURE:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-922-067-1

Query Match 7.9%; Score 186; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 368 MLKLGKGDIDSNAAIDLSNKAFLQKHLGLHKDFDQ 404
|||||
Db 1 MLKLGKGDIDSNAAIDLSNKAFLQKHLGLHKDFDQ 37

RESULT 15
US-10-173-233-1
Sequence 1, Application US/10173233
Publication No. US20030148398A1
GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
Tew, David Graham
Southan, Christopher Donald
Hickey, Dierdre Mary Bernadette
Gloger, Israel Simon
Lawrence, Geoffrey Mark Prouse
Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/173,233
FILING DATE: 14-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/569,899
FILING DATE: 12-May-2000
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
FEATURE:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-173-233-1
Query Match 7.9%; Score 186; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 368 MLKLGKGDIDSNAAIDLSNKAFLQKHLGLHKDFDQ 404
|||||
Db 1 MLKLGKGDIDSNAAIDLSNKAFLQKHLGLHKDFDQ 37

Search completed: March 15, 2005, 10:25:09
Job time : 132.868 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 09:56:51 ; Search time 36.75 Seconds
(without alignments)
1154.601 Million cell updates/sec

Title: US-09-922-067F-14
Perfect score: 2358
Sequence: 1 MPPKLVHLCGCLAVVY.....INTNQHIMLQNSSGIEKYN 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2354	99.8	441	2 S60247	platelet-activatin
2	1572.5	66.7	436	2 JC5021	platelet-activatin
3	497	21.1	384	2 T32756	hypothetical prote
4	493.5	20.9	476	2 T28936	hypothetical prote
5	295.5	12.5	438	2 T39268	hypothetical prote
6	249.5	10.6	450	2 G83740	hypothetical prote
7	162.5	6.9	546	2 D83408	hypothetical prote
8	153.5	6.5	348	2 AB2876	conserved hypothet
9	149	6.3	391	2 T36311	probable lipase -
10	148.5	6.3	795	2 F82858	dipeptidyl-peptida
11	125.5	5.3	395	2 AG2606	conserved hypothet
12	125.5	5.3	395	2 F97388	probable lipase (A
13	125	5.3	545	2 AD2062	hypothetical prote
14	122.5	5.2	275	2 B98301	non-heme chloroper
15	122.5	5.2	275	2 AF2982	non-heme chloroper
16	120.5	5.1	310	2 JN0490	28K lipase precurs
17	120	5.1	543	2 AF1927	hypothetical prote
18	117.5	5.0	622	2 S75452	hypothetical prote
19	116.5	4.9	314	2 AF3193	conserved hypothet
20	112	4.7	286	2 D75217	probable 2-acetyl-
21	110.5	4.7	711	2 S66261	X-Pro dipeptidyl-p
22	110	4.7	622	2 F71174	hypothetical prote
23	108.5	4.6	326	2 T36421	hypothetical prote
24	107	4.5	367	2 S19172	cytochrome P450 2B
25	106.5	4.5	275	2 AB6511	acyltransferase fa
26	106.5	4.5	275	2 G72111	dienelactone hydro
27	106	4.5	632	2 E75057	peptidase PAB1418
28	104.5	4.4	868	2 G82193	aminopeptidase N V
29	103.5	4.4	931	2 A49737	dipeptidyl aminope

30	103.5	4.4	955	2 F84914	hypothetical prote
31	102.5	4.3	248	2 C97652	hypothetical prote
32	102	4.3	275	2 F95848	probable non-heme
33	102	4.3	588	2 D81302	probable ATP/GTP-b
34	101	4.3	335	2 E87625	hypothetical prote
35	101	4.3	390	2 AG1284	cystathionine beta
36	101	4.3	828	2 G87584	hypothetical prote
37	100.5	4.3	338	2 A97914	choline-binding pr
38	100	4.2	793	2 T41703	dipeptidyl aminope
39	99.5	4.2	249	2 AD1051	conserved hypothet
40	99.5	4.2	1010	2 T09499	ATP-dependent clp
41	97.5	4.1	390	2 AB1656	cystathionine beta
42	97.5	4.1	474	2 T15247	hypothetical prote
43	97.5	4.1	538	2 S76481	hypothetical prote
44	97.5	4.1	964	2 A84693	hypothetical prote
45	97.5	4.1	972	2 E84693	hypothetical prote

ALIGNMENTS

RESULT 1

S60247
platelet-activating factor acetylhydrolase precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: S60247
R;Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf, B.; W.
Nature 374, 549-553, (1995)
A;Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase.
A;Reference number: S60247; MUID:95214779; PMID:7700381
A;Accession: S60247
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-441 <TJO>
A;Cross-references: UNIPROT:Q13093; EMBL:U20157; NID:g780132; PIDN:AAC50126.1; PID:g7801

Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 5.1e-178;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MVPPKLVHLCGCLAVVYFDWQYINPVAHMSSAWVNKIQVLMASAFGQTKIPRGN	60
Db	1	MVPPKLVHLCGCLAVVYFDWQYINPVAHMSSAWVNKIQVLMASAFGQTKIPRGN	60
QY	61	GPYSVGCTDLMFHDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI	120
Db	61	GPYSVGCTDLMFHDHTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI	120
QY	121	LRLFGSMTPPANWNSPLRPGKEYPLVVFSGHGLGAFRTLYSAIGIDLASHGFVAAVEHR	180
Db	121	LRLFGSMTPPANWNSPLRPGKEYPLVVFSGHGLGAFRTLYSAIGIDLASHGFVAAVEHR	180
QY	181	DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDDID	240
Db	181	DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDDID	240
QY	241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRFCIALDAWMF	300
Db	241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRFCIALDAWMF	300
QY	301	PLGDEVYSRIPQLFFINSEYFYQPANI IKMKKCYSPDKERKMITIRGSHVQNFAFTFA	360
Db	301	PLGDEVYSRIPQLFFINSEYFYQPANI IKMKKCYSPDKERKMITIRGSHVQNFAFTFA	360
QY	361	TGKIIGHMLKLKGDIDSNAAIDLSNKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT	420
Db	361	TGKIIGHMLKLKGDIDSNVAIDLSNKASLAFQKHLGLHKDFDQWDCLIEGDDENLIPGT	420
QY	421	NINTTNQHIMLQNSSGIEKYN	441
Db	421	NINTTNQHIMLQNSSGIEKYN	441

RESULT 2

JC5021
platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig
N/Alternate names: PAF-acetylhydrolase
C/Species: Cavia porcellus (guinea pig)
C/Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C/Accession: JC5021; PC4207
R/Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoyama, J. Biochem. 120, 838-844, 1996
A/Title: Cloning, expression and characterization of plasma platelet-activating factor-A
A/Reference number: JC5021; MUID:97103479; PMID:8947850
A/Accession: JC5021
A/Molecule type: DNA
A/Residues: 1-436 <KAR1>
A/Cross-references: UNIPROT:P70683; DDBJ:D67037; NID:g1644228; PIDN:BAA11054.1; PID:g1644228
A/Accession: PC4207
A/Molecule type: protein
A/Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392 <KAR1>
A/Experimental source: liver
C/Comment: This enzyme converts platelet-activating factor to an inactive metabolite lysophosphatidic acid
C/Keywords: glycoprotein; hydrolase
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <MAT>
F/76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.7%; Score 1572.5; DB 2; Length 436;
Best Local Similarity 66.2%; Pred. No. 2.5e-116;
Matches 292; Conservative 63; Mismatches 79; Indels 7; Gaps 2;

Qy 1 MVPKHLVFLCLGCLAVVYFDWQYINPVAMKSSAWNKIQVLMMAASFGQTKIPRGN 60
Db 1 MAPPKLHTLFLCLSGFLALVHPFDWRDLDPVYIQSSVWRIQSELLITSFGHTTIPKGN 60

Qy 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMSGYTNQSSFLRYPSQDNDFPDALWIPNEEYFQGLTETLGASSFLGKL 120

Qy 121 LRLFGSMTPPANWNSPLRPGKEYPLVVFSGHGLGAFRTLYSAIGIDLSHGFIIVAAVEHR 180
Db 121 LKLLYGSVKVPKWNPSPLTGEKYPLIIFSHGLGAFRTLYSAIGIELASHGFIIVAAVEHR 180

Qy 181 DRSATYYPKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDLID 240
Db 181 DESAAATYYPQDAPAAESGNRSWIYKV--GNLETEERKQLRQGECSQALSLLSID 238

Qy 241 HGKPVKNALDLKDFMEQLKSDIDREKIAVIGHSGFGGATVIQTLSEDQFRCGIALDWMF 300
Db 239 EGEPVKNVLDLNFIDIQKGLSDRSKVAIGHSGFGGATVIQTLSEDQFRCGIALDWMF 298

Qy 301 PLGDEVSRIPQPLFFINSEYFQYYPANIKMKKCYSPDKERKMITIRGSHQNFADFTFA 360
Db 299 PVGEDVHSKIPQPLFFINSEYFQSANDTKKIEKFYQPKERKMIKGVSVHHNFVDFTFA 358

Qy 361 TGKIIGHMLKLKGDIDSNAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDDENLIPGT 420
Db 359 TGKIIQMLSLKGLKIDSEVAMDLINKASLAFLOKYLGLDKNFDQWNSLMGDDENLIPF 418

Qy 421 NINTTNOHIMLQNSSGIEKYN 441
Db 419 TIPTT-----MQSSTGTQORN 434

RESULT 3

T32756
hypothetical protein W03G9.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T32756
R/Dante, M.; Keppler, D.
submitted to the EMBL Data Library, December 1997
A/Description: The sequence of C. elegans cosmid W03G9.

A/Reference number: Z21220
A/Accession: T32756
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-384 <DAN>
A/Cross-references: UNIPROT:O44753; EMBL:AF039716; PIDN:AAB96738.1; GSPDB:GN00019; CESP:
A/Experimental source: strain Bristol N2; clone W03G9
C/Genetics:
A/Gene: CESP:W03G9.6
A/Map position: 1
A/Introns: 47/3; 90/2; 142/2; 183/3; 333/3

Query Match 21.1%; Score 497; DB 2; Length 384;
Best Local Similarity 33.9%; Pred. No. 1.7e-31;
Matches 118; Conservative 74; Mismatches 140; Indels 16; Gaps 9;

Qy 55 KIPRNGPYSVGCTDLMFHDH-TNKGTFRLRYPSQDNDRDL-----TLWIPNKEYFWGLSK 109
Db 14 KMP---GQPKVGCMDLMIEEAAGSGLFMRLFFPT-DSEITGPSSLPVWIPRPEYAYGVGE 69

Qy 110 FLG-THWLMGNILRLFGSMTPPANWNSPL-RPGEKYPLVVFSGHGLGAFRTLYSAIGIDL 167
Db 70 YLGHSFQMDLISSLVIGDKRVDICIDNAQLSTKSKDWPVLVFSHGLGSGRTFYSTYCTSL 129

Qy 168 ASHGFIIVAAVEHRDRSASATYYPKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAK 227
Db 130 ASHGFIIVAAVEHRDSSACWTYKLVKNGTLVEKPMKIKLVDRNDKQDFKIRNEQVGRKE 189

Qy 228 ECSQALSILDLIDHGKPVKNALDL--KFDMEQLKSDIDREKIAVIGHSGFGGATVIQTLSE 285
Db 190 ECAKAVKILEQLDSGN-VKDKVIIGNNANLEFFKNKLLTTTASIIHSGFGGATSIASSSS 248

Qy 286 DQFRCGIALDAMFPLGDEVSRIPQPLFFINSEYFQYYPANIKMKKCYSPDKERKMIT 345
Db 249 D--FQKAIVLDGWMTPLDONQEQEQAQPIPMFLNVGDWQWNNENLEVMRKILPNNEGNILLT 306

Qy 346 IRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAIDLSNKASLAFLO 393
Db 307 LSGAVHQSFDTDFPFVFPNWLAKQFGVHGPTPEYLCMQSAIELTSLFLK 354

RESULT 4

T28936
hypothetical protein C52B9.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C/Accession: T28936
R/Nelson, J.
submitted to the EMBL Data Library, July 1996
A/Description: The sequence of C. elegans cosmid C52B9.
A/Reference number: Z20545
A/Accession: T28936
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-476 <NEL>
A/Cross-references: EMBL:U64598; PIDN:AAC47973.1; GSPDB:GN00028; CESP:C52B9.7
A/Experimental source: strain Bristol N2; clone C52B9
C/Genetics:
A/Gene: CESP:C52B9.7
A/Map position: X
A/Introns: 23/3; 70/2; 121/3; 164/2; 273/3; 343/3; 425/3

Query Match 20.9%; Score 493.5; DB 2; Length 476;
Best Local Similarity 32.1%; Pred. No. 4.4e-31;
Matches 123; Conservative 69; Mismatches 154; Indels 37; Gaps 8;

Qy 37 AWVNIQVLMMAASFGQTKIPRNGPYSVGCTDLMFHDH---NKGTFRLRYPSQDNDRDL 93
Db 75 SYISSPQVLTROVS-----GQFQVGCCKDLMDGTVLGDRGLFMRLYFPT-DSQAA 123

Qy 94 D-----TLWIPNKEYFWGLSKFLG-THWLMGNILRLFGSMTPPANWNSPLRPG-EKYPLV 147
Db 124 DISSYPLWLPKPQYAHGLGEYLGQSSQKNVITSVVGEKREDCIENAQMSKCKWPIV 183

QY 148 VFSHGLGAPRTLYSAIGIDLASHGFIVAAVEH-----RDRSASATYYFK 191
Db 184 VFSHGLGGSRTFYSTYCTSLASHGYVAAVEHKWKGSGGRCDHVAFSCRDHSACWTYQLT 243

QY 192 DQSAAEIGDKSWLYLRTLKQEEETHIRNEQVQRRAKESQALSILIDIDHGK-PVKNALD 250
Db 244 EKNGELVEQPIKIKLIEKNEKNEFKIRNQVGKRVTECVKALNVLEQLNLGTVPEKVLIG 303

QY 251 LKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDOQRFCGIALDAMFPLGDEVYSRI 310
Db 304 NDYNWAQFNKVLVMSSASVIGHSGFGGATSLASSAYTTDFOKAIVFDGVMVPLDSTQEQEA 363

QY 311 PQLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLK 370
Db 364 KQPTLFLNVGDQWQNNELDVWKKIISHNDGNLALTNGAVHQCFSDFFPFPPSWLAKKFG 423

QY 371 LKGDIDSNAIDLNSKASLAPLQ 393
Db 424 VQGRTEPSLCMQAAIELSLAFLE 446

RESULT 5
T39268
hypothetical protein SPBC106.11c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39268
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21840
A:Accession: T39268
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-438 <LYN>
A:Cross-references: UNIPROT:Q9URV1; EMBL:AL110295; PIDN:CAB53727.1; GSPDB:GN000067; SPDB:
A:Experimental source: strain 972h-; cosmid c106
C:Genetics:
A:Gene: SPDB:SPBC106.11c
A:Map position: 2

Query Match 12.5%; Score 295.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 1.7e-15;
Matches 112; Conservative 84; Mismatches 141; Indels 115; Gaps 22;

QY 55 KIPRNGPYSVG-----CTDLMFDHNTKGTFLRLYY---PSQD-NDRLDTLW 97
Db 10 QLPAYCGPLPVGSLVLELSPVEEFCRCEYKTIHKLRTVKRIFYPPLDPTKDVEPRTDLW 69

QY 98 IPNKEYFWGLSKFLGTHWLMGNILRLFLGSMTPPANWNSPIRPG-----KYPLVVF 149
Db 70 LPFHGIGIPEVAK--GFRWW---LLRAFASGLT---NLALPVYKGELFHPNNGKLPVFIF 121

QY 150 SHGLGAFRTLYSAIGIDLASHGFIVAAVEHRRSA-----SATYFQDQSAE 197
Db 122 SHGLVGSNNVSSLCGTIASYGIIVVLAMEHRDNSAIISTVRDPLHPPEPPYVQYR---E 178

QY 198 IGDKSWLYLRTLKQEEETHIRNEQVQRRAKESQALSILDI-DHGKPVKN-----ALDL 251
Db 179 ISD-----FYADATVVLQNERLLFRQEQIQAQMIRNINDLGTDPENLPFLCSVDS 230

QY 252 KF---DMEQLKDSID--REKIAVIGHSGFGGATV-----IQTLSEDOQRFCGIAL 295
Db 231 SFYNSVFQSMKGNLNTAQGELIVAGHSFGAATCAFISGSSTKSLYNDYMFTEFKCSILY 290

QY 296 DAWMFPLGDEVYSRIPQP-LFFINSEYFQYPANIIKMKCY-----SPDKERK 342
Db 291 DIWMLPVRLHLSTMRYPTLMIISYEFFRFDVNFQALSWLVNKDSENQNASADEKMS 350

QY 343 MITIR-----GSVHQNFADFTFATGKIIGHMLKLKGDIDSNAIDLNSKASLAPLQ 393
Db 351 VVPLKKYSHVFYVDGTVHANQSDLPILLPRMVLRLKGFKEADPYEALRINTRSSVQFLR 410

QY 394 KHLGLHKDFDQWDCLIEGDE-----NLIPG 419
Db 411 EN---HVE-----NVQGDNDPSSLQTNIIPG 433

RESULT 6
G83740
hypothetical protein BH0727 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83740
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, N.; Fujii, F.; Hira-
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G83740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-450 <STO>
A:Cross-references: UNIPROT:Q9KEX2; GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BAB044
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0727

Query Match 10.6%; Score 249.5; DB 2; Length 450;
Best Local Similarity 22.0%; Pred. No. 7.6e-12;
Matches 87; Conservative 75; Mismatches 122; Indels 111; Gaps 16;

QY 56 IPRGNGPYSVGCTDLMF-----DHTNKGTFRLRYPSQ-DNDRDLTLWIPNKEYF 104
Db 112 LPEPTGYEIGVTNFHWDPDREEVEGVNGRELWVRWIWYPAELTEGGLKAPYAFDPSYT 171

QY 105 WGLSKFLGTHWLMGNILRLFLGSMTPPAN--WNSPLRP-GEKYPLVVFVSHGLGAFRTLYS 161
Db 172 ELVSKELPYVY----KALLYSVIQTETHSFANVPVADHGAPYVPLILSPGYGNSNFMYT 226

QY 162 AIGIDLASHGFIVAAVEHRRDRSASATYFQDKQSAAEIGDKSWLYLRTLKQEEETHIRNEQ 221
Db 227 SQAETLASHGYIVCSIEH-----TYV-----TGLPTL--FPDGRIVYEQ 263

QY 222 VRQRAKESQALSILIDIDHGKPVKNAL-----DLKFDMEQLK-----DSIDR 264
Db 264 I-----DLEDGRDLDEEITVWVDDVQFVLDQLQKNESDPQNLLNGRLDM 308

QY 265 EKIAVIGHSGGATVIQTLSEDOQRFCGIALDAMFPLGDEVYSRIPQLFFINS----- 319
Db 309 DRVGMIGHSGFGGATTAQVMHQDPRIRAGVNMDDGLF--GSLIEGLDYPFMYMSGVEVS 366

QY 320 -----EYFQYPANIIKMKKCYSPDKERK-----MITIRGSHVHQNFADFTFAT 361
Db 367 MEGPDGKKVVEAELEP---EFREFIADDKRKEGALKNNGLYVVVIAEHSFSDWMLYS 423

QY 362 GKIIIGHMLKLKGDIDSNAIDLNSKASLAPLQKHL 396
Db 424 PLLLDRDLPM-----LDQINKTLDDFFDEHL 449

RESULT 7
D83408
hypothetical protein PA1907 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: D83408
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho-
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: D83408
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-546 <STO>

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82858
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: F82858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-795 <SIM>
A;Cross-references: UNIPROT:Q9PHC9; GB:AE003856; GB:AE003849; NID:g9104770; PIDN:AAF8282
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0015

Query Match 6.3%; Score 148.5; DB 2; Length 795;
Best Local Similarity 21.1%; Pred. No. 0.0016;
Matches 69; Conservative 50; Mismatches 87; Indels 121; Gaps 16;
QY 108 SKFLGTHWLMGNILRL-----LFGSMTPPANWNSPLRPGSKYPLVVFHSHGLGAFRTL 159
Db 528 STFKAKQWIOPEYVQIPSKHGAGVIWGYGPAS---LQPEKRYPIVMFVHGAGYLQNV 583
QY 160 YSAIGIDLASHGFIVAAVEHRDRSASATYYFKDQSAAEIGDKSWLYLRTLKQEEETHIRN 219
Db 584 -----SARYPSYFREQ-----MFHTLLVQKG----- 604
QY 220 EQVQRRAKESQALSILDID-----HGKPVKNALDLKFDMEQLKDSI----- 262
Db 605 -----YIVLDLDYRASAGHGRDWRRTAIYRNMGHPELEDYLDGLDWLVAHKQ 650
QY 263 -DREKIAVIGHSGG-ATVIOTLSEDRFCRGCIADAWMFPLGDEVYSRIPQPLFFINSE 320
Db 651 GDRRRAGMYGSGYGFMTYMFAPGTGFKAGALR---PVGDWM-----Q 693
QY 321 Y-FQYPANIIKMKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNA 379
Db 694 YNHEYTSNLTNPE-LDPDAYQSSAI-----NYAE-----ALQGHLLILHGMIDNV 740
QY 380 AIDLSNKASLAFLOKHLGHLKDFDQWD 406
Db 741 FF----KOSVDVQKLIELRK--DNWE 761

RESULT 11
AG2606
conserved hypothetical protein Atu0247 [imported] - Agrobacterium tumefaciens (strain C5
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AG2606
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AG2606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <KUR>
A;Cross-references: UNIPROT:Q8UIP6; GB:AE008688; PIDN:AA41269.1; PID:g17738576; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0247
A;Map position: circular chromosome

Query Match 5.3%; Score 125.5; DB 2; Length 395;
Best Local Similarity 24.8%; Pred. No. 0.039;
Matches 54; Conservative 31; Mismatches 66; Indels 67; Gaps 10;
QY 64 SVGCTDLMFDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNILRL 123
Db 63 AVGVSD-----IAHSPDRGKDLAVTIWYP-----SDGKGTQVLSGED-RI 102
QY 124 LFGSMTPPANWNSPLRPGSKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHRDRS 183
Db 103 FQG---TPAFKDAAVQPG-RLPLVLLSHGSGSRVSGMAWIAEKLASEGFIVAGTNHPGTT 158
QY 184 ASATYYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVQRRAKESQALSILDIDHGK 243
Db 159 SG-----DSTPADT-PKIW-----ERTSDLSAIVTAL--TTQ GK 189
QY 244 PVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQ 281
Db 190 -----WSASIDAGRIGVLGFSILGSSAAME 213

RESULT 12
F97388
probable lipase (AL392149) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97388
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97388
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <KUR>
A;Cross-references: UNIPROT:Q8UIP6; GB:AE007869; PIDN:AAK86063.1; PID:g15155138; GSPDB:G
C;Genetics:
A;Gene: AGR_C_423
A;Map position: circular chromosome

Query Match 5.3%; Score 125.5; DB 2; Length 395;
Best Local Similarity 24.8%; Pred. No. 0.039;
Matches 54; Conservative 31; Mismatches 66; Indels 67; Gaps 10;
QY 64 SVGCTDLMFDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNILRL 123
Db 63 AVGVSD-----IAHSPDRGKDLAVTIWYP-----SDGKGTQVLSGED-RI 102
QY 124 LFGSMTPPANWNSPLRPGSKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHRDRS 183
Db 103 FQG---TPAFKDAAVQPG-RLPLVLLSHGSGSRVSGMAWIAEKLASEGFIVAGTNHPGTT 158
QY 184 ASATYYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVQRRAKESQALSILDIDHGK 243
Db 159 SG-----DSTPADT-PKIW-----ERTSDLSAIVTAL--TTQ GK 189
QY 244 PVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQ 281
Db 190 -----WSASIDAGRIGVLGFSILGSSAAME 213

RESULT 13

Db 180 REEFWRQMMGGLKGQLDSIRAFSESD-----FHQDLKAFDKPTLVLHGDDDDQ 227
Qy 416 LIP 418
Db 228 IVP 230

Search completed: March 15, 2005, 10:08:36
Job time : 39.75 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 09:48:35 ; Search time 164.294 Seconds
(without alignments)
1374.528 Million cell updates/sec

Title: US-09-922-067F-14
Perfect score: 2358
Sequence: 1 MVPKXHLVFLCGCLAVVY.....INTTQHIMLQNSSGIEKYN 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2354	99.8	441	1 PAPA_HUMAN	Q13093 h platelet-
2	1964.5	83.3	444	1 PAPA_BOVIN	Q28017 b platelet-
3	1935.5	82.1	444	1 PAPA_CANFA	Q28262 c platelet-
4	1572.5	66.7	436	1 PAPA_CAVPO	P70683 c platelet-
5	1556.5	66.0	440	2 Q921T4	Q921t4 mus musculu
6	1555.5	66.0	440	2 Q8BKM3	Q8bkm3 mus musculu
7	1514.5	64.2	440	1 PAPA_MOUSE	Q60963 m platelet-
8	1226.5	52.0	346	2 Q9DB74	Q9db74 mus musculu
9	1131.5	48.0	422	1 PAPA_CHICK	Q90678 g platelet-
10	1093	46.4	404	2 Q6NYI7	Q6ny17 brachydanio
11	819	34.7	390	1 PAF2_RAT	P83006 rattus norv
12	809	34.3	390	1 PAF2_MOUSE	Q8vvg7 mus musculu
13	797	33.8	392	1 PAF2_HUMAN	Q99487 homo sapien
14	747	31.7	392	1 PAF2_BOVIN	P79106 bos taurus
15	696	29.5	362	2 Q6GPX8	Q6gpx8 xenopus lae
16	508.5	21.6	388	1 PAPA_CAEEL	Q22943 caenorhabdi
17	497	21.1	384	2 Q44753	O44753 caenorhabdi
18	374.5	15.9	103	2 Q6UB75	Q6ub75 sus scrofa
19	308	13.1	609	2 Q7S2B3	Q7s2b3 neurospora
20	296	12.6	920	2 Q7SCR4	Q7scr4 neurospora
21	295.5	12.5	438	2 Q9URV1	Q9urv1 schizosacch
22	249.5	10.6	450	2 Q9KEX2	Q9kex2 bacillus ha
23	220	9.3	468	2 Q6HML0	Q6hml0 bacillus th
24	214	9.1	468	2 Q81UC8	Q81uc8 bacillus an
25	213	9.0	468	2 Q81H53	Q81h53 bacillus ce
26	206.5	8.8	386	2 Q9F2X9	Q9f2x9 streptomyce
27	202	8.6	401	2 Q82QN6	Q82qn6 streptomyce
28	199	8.4	468	2 Q73CM7	Q73cm7 bacillus ce
29	188.5	8.0	456	2 Q81EZ5	Q81ez5 bacillus ce
30	184	7.8	402	2 Q70K06	Q70k06 bacillus am
31	174	7.4	331	2 Q7NJZ2	Q7njz2 gloeobacter

RESULT 1					
PAPA_HUMAN					
ID	PAPA_HUMAN	STANDARD;	PRT;	441	AA.
AC	Q13093; Q15692; Q81VA2;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)				
DE	(PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated				
DE	phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine				
DE	esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).				
GN	Name=PLA2G7; Synonyms=PAPAH;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.				
RC	TISSUE=Myeloid;				
RX	MEDLINE=95214779; PubMed=7700381; DOI=10.1038/374549a0;				
RA	Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,				
RA	Schimpf B., Hooper S., le Trong H., Cousens L.S., Zimmerman G.A.,				
RA	Yamada Y., McInyre T.M., Prescott S.M., Gray P.W.;				
RT	"Anti-inflammatory properties of a platelet-activating factor				
RT	acetylhydrolase.";				
RL	Nature 374:549-553(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	TISSUE=Lymphoma;				
RX	MEDLINE=96197208; PubMed=8624782;				
RA	Tew D.G., Southan C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,				
RA	Moore K., Gloger I.S., Macphie C.H.;				
RT	"Purification, properties, sequencing, and cloning of a lipoprotein-				
RT	associated, serine-dependent phospholipase involved in the oxidative				
RT	modification of low-density lipoproteins.";				
RL	Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).				
RN	[3]				
RP	SEQUENCE FROM N.A., AND VARIANT ALA-379.				
RC	TISSUE=Blood;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Villalon D.K., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				

ALIGNMENTS

Q65iy4 bacillus li
Q82pq3 streptomyce
Q9i2j7 pseudomonas
Q87fb4 xylella faa
Q8ucp7 agrobacteri
Q9z360 streptomyce
Q9phc9 xylella faa
Q8di73 synechococc
Q8xqh7 ralstonia s
Q7uu10 rhodopirell
Q75ci4 ashbya goss
Q728i3 desulfovibr
Q93m73 xanthomonas
Q8p3g3 xanthomonas

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP MUTAGENESIS.
RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H., Zimmerman G.A.,
RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487 (1995).
RN [5]
RP VARIANT PLA2G7 DEFICIENCY PHE-279.
RX MEDLINE=96259525; PubMed=8675689;
RA Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W., Eberhardt C.,
RA Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A., McIntyre T.M.,
RA Gray P.W., Prescott S.M.;
RT "Platelet-activating factor acetylhydrolase deficiency. A missense
RT mutation near the active site of an anti-inflammatory phospholipase.";
RL J. Clin. Invest. 97:2784-2791 (1996).
RN [6]
RP VARIANT PLA2G7 DEFICIENCY ARG-281.
RX MEDLINE=97396177; PubMed=9245731; DOI=10.1006/bbrc.1997.7047;
RA Yamada Y., Yokota M.;
RT "Loss of activity of plasma platelet-activating factor acetylhydrolase
RT due to a novel Gln281-->Arg mutation.";
RL Biochem. Biophys. Res. Commun. 236:772-775 (1997).
RN [7]
RP VARIANT PLA2G7 DEFICIENCY PHE-279.
RX MEDLINE=98074100; PubMed=9412624;
RA Hiramoto M., Yoshida H., Imaizumi T., Yoshimizu N., Satoh K.;
RT "A mutation in plasma platelet-activating factor acetylhydrolase
RT (Val279-->Phe) is a genetic risk factor for stroke.";
RL Stroke 28:2417-2420 (1997).
RN [8]
RP VARIANT PLA2G7 DEFICIENCY PHE-279.
RX MEDLINE=98132308; PubMed=9472966;
RA Yamada Y., Ichihara S., Fujimura T., Yokota M.;
RT "Identification of the G994-->T missense in exon 9 of the plasma
RT platelet-activating factor acetylhydrolase gene as an independent risk
RT factor for coronary artery disease in Japanese men.";
RL Metabolism 47:177-181 (1998).
RN [9]
RP VARIANT PLA2G7 DEFICIENCY PHE-279.
RX MEDLINE=98430412; PubMed=9759612;
RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,
RA Yoshimizu N., Fukushi K., Satoh K.;
RT "A mutation in plasma platelet-activating factor acetylhydrolase
RT (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not
RT for hypertension.";
RL Thromb. Haemost. 80:372-375 (1998).
RN [10]
RP VARIANTS HIS-92; THR-198 AND ALA-379.
RX MEDLINE=20311534; PubMed=10733466;
RA Kruse S., Mao X.-Q., Heinzmann A., Blattmann S., Roberts M.H.,
RA Braun S., Gao P.-S., Forster J., Kuehr J., Hopkin J.M., Shirakawa T.,
RA Deichmann K.A.;
RT "The Ile198Thr and Ala379Val variants of plasmatic PAF-acetylhydrolase
RT impair catalytical activities and are associated with atopy and
RT asthma.";
RL Am. J. Hum. Genet. 66:1522-1530 (2000).
CC -1- FUNCTION: Modulates the action of platelet-activating factor (PAF)
CC by hydrolyzing the sn-2 ester bond to yield the biologically
CC inactive lyso-PAF. Has a specificity for substrates with a short
CC residue at the sn-2 position. It is inactive against long-chain
CC phospholipids.
CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Plasma.

CC -1- POLYMORPHISM: The alleles Thr-198 and Val-379 are associated with
CC atopy and asthma.
CC -1- DISEASE: Defects in PLA2G7 are the cause of platelet-activating
CC factor acetylhydrolase deficiency (PLA2G7 deficiency)
CC [MIM:601690]. It is a trait which is present in 2% of Japanese.
CC It could have a significant physiologic effect in the presence of
CC inflammatory bodily responses.
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U20157; AAC50126.1; --
CC EMBL; U24577; AAB04170.1; --
CC EMBL; BC038452; AAH38452.1; --
CC PIR; S60247; S60247.
CC Genew; HGNC:9040; PLA2G7.
CC MIM; 601690; --
CC GO; GO:0005576; C:extracellular; TAS.
CC GO; GO:0005543; F:phospholipid binding; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0006629; P:lipid metabolism; TAS.
CC InterPro; IPR008262; Lipase AS.
CC InterPro; IPR005065; PAF_Ac_hydrolase II.
CC InterPro; IPR000379; Ser_estr.
CC Pfam; PF03403; PAF-AH_p II; 1.
CC PROSITE; PS00120; LIPASE_SER; 1.
CC Direct protein sequencing; Disease mutation; Glycoprotein; Hydrolase;
CC Lipid degradation; Polymorphism; Signal.
CC SIGNAL 1 21
CC CHAIN 22 441 Platelet-activating factor
CC ACT_SITE 273 273 acetylhydrolase.
CC ACT_SITE 296 296 Charge relay system.
CC ACT_SITE 351 351 Charge relay system.
CC CARBOHYD 423 423 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 433 433 N-linked (GlcNAc...)
CC VARIANT 92 92 R -> H (common polymorphism;
CC dbSNP:1805017).
CC VARIANT 198 198 /FTID=VAR_011583.
CC VARIANT 279 279 I -> T (common polymorphism;
CC dbSNP:1805018).
CC VARIANT 279 279 /FTID=VAR_011584.
CC VARIANT 281 281 V -> F (in PLA2G7 deficiency; loss of
CC function; more common among Japanese than
CC in Caucasians; risk factor for coronary
CC artery disease and stroke).
CC VARIANT 281 281 /FTID=VAR_004268.
CC VARIANT 379 379 Q -> R (in PLA2G7 deficiency; loss of
CC function).
CC VARIANT 379 379 /FTID=VAR_011585.
CC VARIANT 108 108 V -> A (common polymorphism;
CC dbSNP:1051931).
CC MUTAGEN 108 108 /FTID=VAR_011586.
CC MUTAGEN 273 273 S->A: Activity is higher than wild type.
CC MUTAGEN 286 286 S->A: Loss of activity.
CC MUTAGEN 286 286 D->A: Almost no activity.
CC MUTAGEN 296 296 D->N: Diminished activity.
CC MUTAGEN 296 296 D->A: Loss of activity.
CC MUTAGEN 304 304 D->N: Loss of activity.
CC MUTAGEN 338 338 D->A: No change in activity.
CC MUTAGEN 351 351 D->A: Activity is higher than wild type.
CC MUTAGEN 351 351 H->A: Loss of activity.
CC SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;
CC Query Match 99.8%; Score 2354; DB 1; Length 441;
CC Best Local Similarity 99.8%; Pred. No. 1.3e-174;

Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVPPKLVLCGCLAVVYFDWQYINPVAMKSSAWNKIQVLMAAASFQGTIPRGN 60
Db 1 MVPPKLVLCGCLAVVYFDWQYINPVAMKSSAWNKIQVLMAAASFQGTIPRGN 60

QY 61 GPYSVGCTDLMPDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMPDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120

QY 121 LRLFLGSMTPPANWNSPLRPGKYPVLVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFLGSMTPPANWNSPLRPGKYPVLVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

QY 181 DRSASATYFFKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDI 240
Db 181 DRSASATYFFKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDI 240

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQFRFCGIALDAWMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQFRFCGIALDAWMF 300

QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTFA 360
Db 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTFA 360

QY 361 TGKIIIGHMLKLKGDIDSNAADLSNKAFLQKHLGLHGFQDQDCLIEGDDENLIPGT 420
Db 361 TGKIIIGHMLKLKGDIDSNAADLSNKAFLQKHLGLHGFQDQDCLIEGDDENLIPGT 420

QY 421 NINTTNQHIMLQNSSGIEKYN 441
Db 421 NINTTNQHIMLQNSSGIEKYN 441

RESULT 2

PAFA_BOVIN

ID PAFA_BOVIN STANDARD; PRT; 444 AA.

AC Q28017;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)

DE (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetyl-1-alkylglycerophosphocholine esterase).

GN Name=PLA2G7;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;

RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A., McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;

RA "Plasma platelet-activating factor acetylhydrolase is a secreted phospholipase A2 with a catalytic triad."

RL J. Biol. Chem. 270:25481-25487(1995).

CC -!- FUNCTION: Modulates the action of platelet-activating factor (PAF) by hydrolyzing the sn-2 ester bond to yield the biologically inactive lyso-PAF. Has a specificity for substrates with a short residue at the sn-2 position. It is inactive against long-chain phospholipids.

CC -!- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine + H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: Plasma.

CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; U34247; AAC48483.1; --

DR InterPro; IPR008262; Lipase AS.

DR InterPro; IPR005065; PAF_Ac_hydrolase II.

DR InterPro; IPR000379; Ser_estra.

DR Pfam; PF03403; PAF-AH_p_II; 1.

DR PROSITE; PS00120; LIPASE_SER; 1.

KW Glycoprotein; Hydrolase; Lipid degradation; Signal.

FT SIGNAL 1 21 By similarity.

FT CHAIN 22 444 Platelet-activating factor acetylhydrolase.

FT ACT_SITE 274 274 Charge relay system (By similarity).

FT ACT_SITE 297 297 Charge relay system (By similarity).

FT ACT_SITE 352 352 Charge relay system (By similarity).

FT CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 424 424 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 434 434 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 444 AA; 50133 MW; 97689917BE2F4C38 CRC64;

Query Match 83.3%; Score 1964.5; DB 1; Length 444;

Best Local Similarity 82.4%; Pred. No. 2.6e-144;

Matches 364; Conservative 39; Mismatches 38; Indels 1; Gaps 1;

QY 1 MVPPKLVLCGCLAVVYFDWQYINPVAMKSSAWNKIQVLMAAASFQGTIPRGN 60
Db 1 MLPSKLVLCGCLAVVYFDWQYINPVAMKSSAWNKIQVLMAAASFQGTIPRGN 60

QY 61 GPYSVGCTDLMPDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMPDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120

QY 121 LRLFLGSMTPPANWNSPLRPGKYPVLVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 MGLFFGSMTPPANWNSPLRPGKYPVLVFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

QY 181 DRSASATYFFKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDI 239
Db 181 DGSASATYFFKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILDI 240

QY 240 DHGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQFRFCGIALDAWM 299
Db 241 DHGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDQFRFCGIALDAWM 300

QY 300 FPLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTF 359
Db 301 FPLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTF 360

QY 360 ATGKIIGHMLKLKGDIDSNAADLSNKAFLQKHLGLHGFQDQDCLIEGDDENLIPG 419
Db 361 ATGKIIGHMLKLKGDIDSNAADLSNKAFLQKHLGLHGFQDQDCLIEGDDENLIPG 420

QY 420 TNINTTNQHIMLQNSSGIEKYN 441
Db 421 TNINTTNQHIMLQNSSGIEKYN 442

RESULT 3

PAFA_CANFA

ID PAFA_CANFA STANDARD; PRT; 444 AA.

AC Q28262;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)

DE (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated


```
FT ACT_SITE 271 271 acetylhydrolase.
FT ACT_SITE 294 294 Charge relay system (By similarity).
FT ACT_SITE 349 349 Charge relay system (By similarity).
FT CARBOHYD 76 76 Charge relay system (By similarity).
FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 436 AA; 49062 MW; C359D96B392FFE11 CRC64;

Query Match 66.7%; Score 1572.5; DB 1; Length 436;
Best Local Similarity 66.2%; Pred. No. 8.1e-114;
Matches 292; Conservative 63; Mismatches 79; Indels 7; Gaps 2;

QY 1 MYPKLVHLCGCLAVVYFDFWQYINPVAMKSSAWNKIQVLMASAFGQTKIPRGN 60
Db 1 MAPPKLVHLCGCLAVVYFDFWQYINPVAMKSSAWNKIQVLMASAFGQTKIPKGN 60

QY 61 GPYSVGCTDLMPDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMSGYTNQSFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120

QY 121 LRLFGSMTTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LKLLYGSVKVPKWNKSPKGTGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

QY 181 DRASATYFFKDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDDID 240
Db 181 DESAATYFFQDAPAAESGNRSWYIKV--GNLETEERKRLQRGECSQALSILDDID 238

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRRCGIALDWMF 300
Db 239 EGEPVKNVLDNFIDIOQLKGLDRSKVAIGHSGFGGATVIQTLSEDFRRCGIALDWMF 298

QY 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSHVHNFADTFEA 360
Db 299 PVGEDVHSKIPQPLFFINSEYFQSANDTKKIEKFYQPKERKMIKVGSHVHNFVDFTEA 358

QY 361 TGKIIIGHMLKLKGDIDSNAAIDLSNKASLAFLOKHLGKDFDQDWDCLIEGDDENLIPGT 420
Db 359 TGKIIIGMLSLKGIKIDSEVAMDLINKASLAFLOKHLGKDFDQDWDCLIEGDDENLIPGF 418

QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 419 TIPTT-----MQSSTGTQORN 434

RESULT 5
Q921T4 ID Q921T4 PRELIMINARY; PRT; 440 AA.
AC Q921T4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phospholipase A2, group VII (Platelet-activating factor
GN Name=Pla2g7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
```

```
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010726; AAH10726.1; -.
DR MGD; MGI:1351327; Pla2g7.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR Pfam; PF03403; PAF-AH_P_II; 1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 440 AA; 49230 MW; 17C8B4D28F085794 CRC64;

Query Match 66.0%; Score 1556.5; DB 2; Length 440;
Best Local Similarity 67.1%; Pred. No. 1.4e-112;
Matches 296; Conservative 55; Mismatches 89; Indels 1; Gaps 1;

QY 1 MYPKLVHLCGCLAVVYFDFWQYINPVAMKSSAWNKIQVLMASAFGQTKIPRGN 60
Db 1 MVPLKQLALFCLLCCLPWVHPFWQDTSSF-DFRPSVMFHKLQSVMSAAGSHSKIPKGN 59

QY 61 GPYSVGCTDLMPDHTNKGTFRLYYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 60 GSYVPVGCTDLMPGYGNESVFLYYPAQDQGRDLTLWIPNKEYFLGLSIFLGTSPSIVGNI 119

QY 121 LRLFGSMTTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 120 LHLLYGSLLTPASWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVATVEHR 179

QY 181 DRASATYFFKDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKECSQALSILDDID 240
Db 180 DRASATYFFEDQVAAKVENRSWLYLRKVQKEESESVRKEQVQORAIECSALSAILDIE 239

QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRRCGIALDWMF 300
Db 240 HGDPKENVLGSADFMDKQLKDAIDETKIALMGHSFGGATVQLALSEDFRRCGVALDPWY 299

QY 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSHVHNFADTFEA 360
Db 300 PVNEELYSRTLOPLLFINSKAFQTPKDIKMKKFFQPKERKMITIKGSHVHNFDDFTFV 359

QY 361 TGKIIIGHMLKLKGDIDSNAAIDLSNKASLAFLOKHLGKDFDQDWDCLIEGDDENLIPGT 420
Db 360 TGKIIIGNKLTGKEIDSRVAIDLTKASNAFLQKHLGKDFDQDWDPLVEGDDENLIPGS 419

QY 421 NINTTNOHIMLQNSSGIEKYN 441
Db 420 PFDAVTQAPAQHSPGSGTQN 440

RESULT 6
Q98KM3 ID Q98KM3 PRELIMINARY; PRT; 440 AA.
AC Q98KM3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
DE enriched library, clone:D130049018 product:phospholipase A2 group VII
DE (platelet-activating factor acetylhydrolase, plasma), full insert
DE sequence.
```

GN Name=Pla2g7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK051454; BAC34647.1; -.
DR MGD; MGI:1351327; Pla2g7.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR005065; PAF_Ac_hydrolase II.
DR InterPro; IPR000379; Ser_estra.
DR Pfam; PF03403; PAF-AH_P_II; 1.

DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 440 AA; 49258 MW; 17C8B4D28F1ADC94 CRC64;

Query Match 66.0%; Score 1555.5; DB 2; Length 440;
Best Local Similarity 67.1%; Pred. No. 1.7e-112;
Matches 296; Conservative 55; Mismatches 89; Indels 1; Gaps 1;

Qy 1 MVPPKLHVLFCGCLAVVYFEDWQVYINPVAHMKSAAWVNKIQVLMMAASFGQTKIPRGN 60
Db 1 MVPLKQALFCLLCCLPWVHPFHWDTSF-DPRSPVMFHKLQSVMSAAGSGHSKIPKGN 59

Qy 61 GPYSVGCTDLMFEDHTNKGTFRLRYYPQDNDRDLTIWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 60 GSYPVGCTDLMFYGNESVFVRLYYPAQDQGRDLTIWIPNKEYFLGLSIFLGTSPSIVGNI 119

Qy 121 LRLLEGSMTTPANWNSPLRPGEKYPVLFVFSHGLGAPRTLYSAIGIDLASHGFIVAAVEHR 180
Db 120 LHLLYGSLLTPASWNSPLRTGEKYPVLFVFSHGLGAPRTIYSAIGIGLASNGFIVATVEHR 179

Qy 181 DRASATYYFKDQSAABIGDKSWLYLRTLKOEETHIRNEQVRQRAKESQALSLLILDID 240
Db 180 DRASATYFFEDQVAAKVENRSLYLRKVQEESESVRKEQVQQRRAIECSRALSAILDIE 239

Qy 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDFRCGIALDAWMF 300
Db 240 HGDPEENVLGSADFDMKQLKDAIDETKIALMGHSGFGATVLQALSEDFRCGVALDPWY 299

Qy 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHQNFADTFE 360
Db 300 PVNEELYSRTLQPLLFINSKFTQPKDIKMKKFPQDKERKMITIKGSHQNFDDTFV 359

Qy 361 TGKIIGHMLKLKGDIDSNAAIDLSNKASLAFLOKHLGHKDFDQWPCLEGGDENLIPGT 420
Db 360 TGKIIGNKLTLLKGEIDSRVAIDLTKASMAFLQHLGLQKDFDQWPLVEGGDENLIPGS 419

Qy 421 NINTTNOHIMLQNSSGIEKYN 441
Db 420 PFDAVTQVPAQQHSPGSQTQN 440

RESULT 7
PAPA_MOUSE
ID PAPA_MOUSE STANDARD; PRT; 440 AA.
AC Q60963;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated
DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
DE esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).
GN Name=Pla2g7; Synonyms=Pafah;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H., Zimmerman G.A.,
RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
phospholipase A2 with a catalytic triad.";
RL J. Biol. Chem. 270:25481-25487(1995).
CC -!- FUNCTION: Modulates the action of platelet-activating factor (PAF)
CC by hydrolyzing the sn-2 ester bond to yield the biologically
CC inactive lyso-PAF. Has a specificity for substrates with a short
CC residue at the sn-2 position. It is inactive against long-chain
CC phospholipids.
CC -!- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.

CC -|- SUBCELLULAR LOCATION: Extracellular.
CC -|- TISSUE SPECIFICITY: Plasma.
CC -|- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U34277; AAC52274.1; --.
DR MGD; MGI:1351327; Pla2g7.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR005065; PAF_Ac_hydrolase_II.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF03403; PAF-AH_p_II; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Glycoprotein; Hydrolase; Lipid degradation; Signal.
FT SIGNAL 1 21 By similarity.
FT CHAIN 22 440 Platelet-activating factor
acetylhydrolase.
FT ACT_SITE 272 272 Charge relay system (By similarity).
FT ACT_SITE 295 295 Charge relay system (By similarity).
FT ACT_SITE 350 350 Charge relay system (By similarity).
FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 75 75 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 199 199 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 440 AA; 49361 MW; C82A68AD42F482EB CRC64;

Query Match 64.2%; Score 1514.5; DB 1; Length 440;
Best Local Similarity 65.8%; Pred. No. 2.7e-109;
Matches 290; Conservative 55; Mismatches 95; Indels 1; Gaps 1;

QY 1 MVPPKLVFLCLCGCLAVVYFDPDQYINPVVHMKSSAWNKIQVLMMAASFQGTKIPRGN 60
Db 1 MVPLKQLALFCLLCCLPWVHPFHQDTSF-DPRPSVMFHLQSVMSAAGSHSKIPKGN 59

QY 61 GPYSVGCTDLMPDHTNKGTLRLYPSODNDRDLTLWIPNKEYFWGLSKPLGTHWLMGNI 120
Db 60 GSYVPGCTDLMPFGYGNESVFRLYYPAQDQGRDLTVWIPNKEYFLGLSIFLGTSPVIGNI 119

QY 121 LRLFGSMTPPTANMNSPLRPGSKYPLVVFSGHGFATRLYSAGIDLASHGFIIVAAVEHR 180
Db 120 LHLLYGLSLTTPASWNSPLRTGKPYPLVVFSGHGFATRLYSAGIGLASNGFIVATVEHR 179

QY 181 DRSASATYFFKQDSAAEIGDKSWLYLRTLKQBEETHIRNEQVQRQAKESQALSILDDID 240
Db 180 DRSASATYFFEDQVAAKVENRWLYLRKVQBESESVRKEQVQVQRAIECSRALSAILDIE 239

QY 241 HGKPVKNALDLKPDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDOFRFCGIALDAWMF 300
Db 240 HGDPKENVLGSADFDMKQLKDAIDETKIALMGHSGFGATVLQALSEDOFRFCGVALDPWY 299

QY 301 PLGDEVYSRIPQPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSHVQNFADTFEA 360
Db 300 PVNEELYSRTLQPLLLFINSKAFQTPKDIAMKFFQPDKERKNDYNQGLRHQNFDDTFV 359

QY 361 TGKLIIGHMLKLGDDIDSNAADLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 360 TGKLIIGNKLTGKEIDSRVAIDLTKNASMAFLQKHLGLQKDFDQWDLVLEGDDENLIPGS 419

QY 421 NINTNQHIMLQNSSGIEKYN 441
Db 420 PFDVAVTQAPAQOHSPGSQTQN 440

RESULT 8
Q9DB74 PRELIMINARY; PRT; 346 AA.
ID Q9DB74
AC Q9DB74;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched
DE library, clone:150005E13 product:phospholipase A2 group VII
DE (platelet-activating factor acetylhydrolase, plasma), full insert
DE sequence.
GN Name=Pla2g7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/350555500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Furukishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK005158; BAB23849.1; --.

Qy	71	MPDHTNKGTFRLIYYP-SQDNDRDLTLWIPNKEYFWGLSKFLGTHW---LMGNILRLLLFG	126
Db	1	MVGHSGEGSFFRLFYPCGSSHDVQYPMWLPSEYVVTALAKYLG--WDSSITYISSLIIFG	58
Qy	127	SMTTPANWNSPLRPG-EKYPLVVFESHGLGAFRTLYSAIGIDLASHGFIVAAVEHRDRSAS	185
Db	59	HPQVPVPWSAPFVTGVDDKKPLIIFSHGLGAFRTVYSALCMQLASHGFLVALEHRDGSAC	118
Qy	186	ATYYFKDQ-----SAAEIGDKSWLYLRTLKQEEETHIRNEQVQRACECSQ	231
Db	119	ATYHFADDDPTNAPLKEVWVPFSKVEVGMK-----EFYLRNYQLHHRANECVR	166
Qy	232	ALSLILDIDHGPVKNALDLKEDMEQLKDSIDREKIAVIGHSGGATVIQTLSEDOFRFC	291
Db	167	VMQILRDINAG-VFENVLKSDFDLQALKGRMDPNVVAIMGHSFGGASTLLSLAKDDTFC	225
Qy	292	GIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSVH	351
Db	226	AIALDAMFPLEDASYTNIQKPLIFINAEHFQTTSSIQKMKRLNAGNRESKAITILGSVH	285
Qy	352	QNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLIE	410
Db	286	HSLSDSAFLSGFLADRILOPRAKLNPEOCLQATITSALSFLQKHLDLPGNIPSLDSLSE	344

Search completed: March 15, 2005, 10:07:38
Job time : 167.294 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 09:47:50 ; Search time 64.2647 Seconds
(without alignments)
1029.119 Million cell updates/sec

Title: US-09-922-067F-14_COPY_271_441
Perfect score: 912
Sequence: 1 GHSFGGATVIQTLSEDRFR.....INTTQHIMLQNSSGIEKYN 171

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	912	100.0	441	3 AAB01942	Aab01942 Human low
2	912	100.0	441	5 AAE14750	Aae14750 Human lip
3	912	100.0	442	2 AAR64928	Aar64928 Human T-c
4	908	99.6	400	7 ADG73660	Adg73660 Human PAF
5	908	99.6	440	4 AAE00782	Aae00782 Mouse-Hum
6	908	99.6	440	4 AAE00783	Aae00783 Mouse-Hum
7	908	99.6	441	2 AAR71913	Aar71913 Human pla
8	908	99.6	441	2 AAR73046	Aar73046 Human ace
9	908	99.6	441	2 AAR73047	Aar73047 Human ace
10	908	99.6	441	2 AAR71920	Aar71920 Human ace
11	908	99.6	441	2 AAW23796	Aaw23796 Human pla
12	908	99.6	441	2 AAW09808	Aaw09808 Platelet-
13	908	99.6	441	2 AAW26498	Aaw26498 Human pla
14	908	99.6	441	2 AAW38361	Aaw38361 Human pla
15	908	99.6	441	2 AAW96334	Aaw96334 Human pla
16	908	99.6	441	2 AAW73359	Aaw73359 Human PAF
17	908	99.6	441	3 AAY88301	Aay88301 Human pla
18	908	99.6	441	3 AAY50735	Aay50735 Human PAF
19	908	99.6	441	3 AAB07774	Aab07774 Plasma pl
20	908	99.6	441	4 AAE00761	Aae00761 Human pla
21	908	99.6	441	4 AAE00777	Aae00777 Human pla
22	908	99.6	441	4 AAE00768	Aae00768 Human pla
23	908	99.6	441	4 AAE00778	Aae00778 Human pla
24	908	99.6	441	4 AAB49451	Aab49451 Platelet-
25	908	99.6	441	4 AAE15515	Aae15515 Human pla

26	908	99.6	441	4 AAE15524	Aae15524 Human pla
27	908	99.6	441	4 AAE15525	Aae15525 Human pla
28	908	99.6	441	4 AAE15507	Aae15507 Human pla
29	908	99.6	441	5 ABG61862	Abg61862 Prostate
30	908	99.6	441	6 ABP55072	Abp55072 Human lip
31	908	99.6	441	6 ADA19491	Ada19491 Human pla
32	908	99.6	441	7 ADP65141	Adp65141 Human pho
33	908	99.6	441	8 ADJ57408	Adj57408 Human pho
34	908	99.6	441	8 ADP12938	Adp12938 Protein e
35	908	99.6	441	8 ADR14277	Adr14277 Human NF-
36	908	99.6	441	8 ADR51543	Adr51543 Human lip
37	908	99.6	441	8 ADP54611	Adp54611 Human PRO
38	908	99.6	441	8 ADP23967	Adp23967 PRO polyP
39	908	99.6	520	7 ADG73668	Adg73668 Human hCB
40	908	99.6	638	7 ADG73670	Adg73670 Human gCB
41	908	99.6	642	7 ADG73672	Adg73672 Human aCB
42	905	99.2	441	2 AAR71921	Aar71921 Human ace
43	905	99.2	441	4 AAE00769	Aae00769 Human pla
44	905	99.2	441	4 AAE15516	Aae15516 Human pla
45	903	99.0	441	4 AAE00771	Aae00771 Human pla

ALIGNMENTS

RESULT 1
AAB01942
ID AAB01942 standard; protein; 441 AA.
XX
AC AAB01942;
XX
DT 18-SEP-2000 (first entry)
XX
DE Human low density lipoprotein-associated phospholipase A2 (LDL-PLA2).
XX
KW Human; low density lipoprotein associated phospholipase A2; LDL-PLA2;
KW plasma PAF acetyl hydroxylase; recombinant; purification;
KW short chain phospholipid; serine-dependant phospholipase; inflammation;
KW proinflammatory; anti inflammatory; drug screening; antibody; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200024910-A1.
XX
PD 04-MAY-2000.
XX
PF 27-OCT-1999; 99WO-GB003551.
XX
PR 28-OCT-1998; 98GB-00023647.
PR 28-OCT-1998; 98GB-00023648.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Boyd H, Tew DG;
XX
DR WPI; 2000-350749/30.
DR N-PSDB; AAA52357.
XX
PT Recombinant low density lipoprotein associated phospholipase A2, used to
PT produce antibodies for diagnostics, is purified using a Blue Sepharose
PT and Q Sepharose column.
XX
PS Claim 6b; Page 17; 28pp; English.
XX
CC The present sequence represents human LDL-PLA2. The invention relates to
CC a method for purifying recombinant low density lipoprotein- associated
CC phospholipase A2 (LDL-PLA2). The method comprises applying a cell
CC extract, supernatant or solution containing the recombinantly expressed
CC LDL-PLA2 to a zinc chelating column, applying the eluate to a Blue
CC Sepharose column, and applying that eluate to a Q Sepharose column. The
CC invention also provides a process which additionally comprises the prior
CC steps of constructing a vector comprising a cDNA encoding a histidine
CC tagged LDL-PLA2 or fragment thereof, expressing the tagged protein in a

CC	host cell, isolating the tagged protein from the harvest medium or cell
CC	lysate, purifying the protein using a metal matrix affinity column
CC	(preferably a nickel column), and removing the histidine tag by protease
CC	cleavage. LDL-PLA2, also known as plasma PAF acetyl hydroxylase, is a
CC	serine-dependent phospholipase which catalyses the hydrolysis of
CC	phospholipids with short chain acyl groups at the sn-2 position. Its in
CC	vivo role is not known - due to its ability to hydrolyse both
CC	phospholipids with short chain sn-2 substituents (which often arise from
CC	oxidative cleavage of longer chain sn-2 substituents) and PAF, it may be
CC	either a pro-inflammatory enzyme or an anti-inflammatory enzyme,
CC	depending on the precise in vivo role adopted. LDL-PLA2 can be used in
CC	structural and mechanistic studies to elucidate the activity of the
CC	enzyme in vivo. The enzyme may be used to screen and identify compounds
CC	which modulate its activity, and to raise antibodies for use in
CC	diagnostics
XX	
SQ	Sequence 441 AA;
	Query Match 100.0%; Score 912; DB 3; Length 441;
	Best Local Similarity 100.0%; Pred. NO. 2.5e-98;
	Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 GHSFGGATVIQTLSEDRFRGCIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db	271 GHSFGGATVIQTLSEDRFRGCIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
QY	61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKA 120
Db	331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKA 390
QY	121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTNQHIMLQNSSGIEKYN 171
Db	391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTNQHIMLQNSSGIEKYN 441
RESULT 2	
AAEI4750	
ID	AAEI4750 standard; protein; 441 AA.
XX	
AC	AAEI4750;
XX	
DT	04-OCT-2002 (first entry)
XX	
DE	Human lipoprotein-associated phospholipase A2.
XX	
KW	Atherosclerosis; single nucleotide polymorphism; SNP;
KW	lipoprotein-associated phospholipase A2; Lp-PLA2; human.
XX	
OS	Homo sapiens.
XX	
PN	WO200236817-A2.
XX	
PD	10-MAY-2002.
XX	
PF	02-NOV-2001; 2001WO-GB004876.
XX	
PR	04-NOV-2000; 2000GB-00027181.
XX	
PA	(SMIK) SMITHKLINE BEECHAM PLC.
XX	
PI	Campbell D, McGinnins R, Spurr N, Valdes AM;
XX	
DR	WPI; 2002-479764/51.
DR	N-PSDB; AAD36733.
XX	
PT	Diagnosing atherosclerosis or predicting susceptibility of a subject to
PT	atherosclerosis by determining single nucleotide polymorphism in Lp-PLA2-
PT	encoding polynucleotide.
XX	
PS	Disclosure; Page 14; 30pp; English.
XX	
CC	The invention relates to a method of diagnosing atherosclerosis or
CC	predicting the susceptibility of a subject to atherosclerosis, comprising

determining the presence or absence of a single nucleotide polymorphism (SNP) in codon 379 of a lipoprotein-associated phospholipase A2 (Lp-PLA2) -encoding polynucleotide, where the codon comprising the SNP encodes an amino acid other than valine. The method is useful for predicting the likelihood of developing atherosclerosis, predicting and responding to the progression of the atherosclerotic condition and drug treatment, or predicting disease outcome in a subject. The method is also useful in the selection of patient groups for conducting clinical trials concerning therapeutic compounds with potential for use in the treatment of atherosclerosis. The present sequence is human lipoprotein-associated phospholipase A2

CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

Sequence 441 AA;

Query Match 100.0%; Score 912; DB 5; Length 441;
Best Local Similarity 100.0%; Pred. NO. 2.5e-98;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSFGGATVIOTLSEDOFRFCGIALDAWMFPLGDEVYSRIPQLFFFINSEYFOYPANIIK 60
DB 271 GHSFGGATVIOTLSEDOFRFCGIALDAWMFPLGDEVYSRIPQLFFFINSEYFOYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIIGHMLKLKGDIDSNAAIDLSENKASLA 120
DB 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIIGHMLKLKGDIDSNAAIDLSENKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEIGDDENLIPGTNTNTNQHIMLQNSSGIEKYN 171
DB 391 FLQKHLGLHKDFDQWDCLEIGDDENLIPGTNTNTNQHIMLQNSSGIEKYN 441

RESULT 3
AAR64928
ID AAR64928 standard; protein; 442 AA.
XX
AC AAR64928;
XX
DT 25-MAR-2003 (revised)
DT 18-AUG-1995 (first entry)
XX
DE Human T-cell lymphoma lipoprotein-associated phospholipase-A2.
XX
KW T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2; enzyme;
KW atherosclerosis; diagnosis; therapy; antiarteriosclerotic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 25. .31
FT /note= "Peptide 4"
FT Peptide 115. .133
FT /note= "Peptide 3"
FT Peptide 298. .327
FT /note= "Peptide 2"
FT Peptide 368. .393
FT /note= "Peptide 1"
XX
PN WO9500649-A1.
XX
XX
PD 05-JAN-1995.
XX
PF 24-JUN-1994; 94WO-GB001374.
XX
PR 25-JUN-1993; 93GB-00013144.
PR 11-JAN-1994; 94GB-00000413.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Macphee CH, Tew DG, Southan CD, Hickey DMB, Gloger IS;
PI Lawrence GMP, Rice SQJ;
XX
DR WPI; 1995-052086/07.
DR N-PSDB; AAQ81780.

XX Purified lipoprotein associated phospholipase A2 - used to develop prods.
PT for diagnosis and therapy, partic. inhibitors for treatment of
PT atherosclerosis.
XX Claim 8; Page 19; 29pp; English.
PS This sequence encodes an enzyme which may be used in a method of
XX screening compounds to identify those compounds which inhibit Lp-PLA2
CC which involves contacting isolated Lp-PLA2 with a test compound and
CC measuring the rate of turnover of an enzyme substrate as compared with
CC the rate of turnover in the absence of the test compound. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX Sequence 442 AA;
SQ Query Match 100.0%; Score 912; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.5e-98;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 330
Qy 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKGDIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKGDIDSNAAIDLSNKASLA 390
Qy 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 441
RESULT 4
ADG73660
ID ADG73660 standard; protein; 400 AA.
XX
AC ADG73660;
XX
DT 11-MAR-2004 (first entry)
XX
DE Human PAF-AH SEQ ID NO:8.
XX
KW collagenase; collagen; platelet activating factor; acetyl hydrolase;
KW collagen coupling region; antiinflammatory; inflammation;
KW skin transplantation; human.
XX
OS Homo sapiens.
XX
PN JP2003284553-A.
XX
PD 07-OCT-2003.
XX
PF 28-MAR-2002; 2002JP-00090847.
XX
PR 28-MAR-2002; 2002JP-00090847.
XX
PA (SEK) SEIKAGAKU KOGYO CO LTD.
XX
XX WPI; 2003-869686/81.
DR N-PSDB; ADG73659.
XX
XX Novel bioactive protein binding with collagen and having platelet
PT activating factor and acetyl hydrolase activity, useful for suppressing
PT local inflammation.
XX
PS Claim 2; SEQ ID NO 8; 53pp; Japanese.
XX
CC The invention relates to a novel bioactive protein binding with collagen
CC having platelet activating factor and acetyl hydrolase activity, and
CC comprising collagen coupling region. A protein of the invention has
CC antiinflammatory activity. A protein of the invention is useful for
CC suppressing local inflammation caused during skin transplantation. The

CC present sequence is used in the exemplification of the invention.
XX Sequence 400 AA;
SQ Query Match 99.6%; Score 908; DB 7; Length 400;
Best Local Similarity 99.4%; Pred. No. 6.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db 230 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 289
Qy 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKGDIDSNAAIDLSNKASLA 120
Db 290 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKGDIDSNVAIDLSNKASLA 349
Qy 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db 350 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 400
RESULT 5
AAE00782
ID AAE00782 standard; protein; 440 AA.
XX
AC AAE00782;
XX
DT 11-SEP-2003 (revised)
DT 02-JUL-2001 (first entry)
XX
DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC1.
XX
KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
KW antiinflammatory; septicaemia; inflammation; haemostasis; parturition;
KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..97
FT /note= "Corresponds to N-terminal 97 amino acids of mouse
FT plasma platelet-activating factor acetylhydrolase (PAF-
FT AH)"
FT Region 98..440
FT /note= "Corresponds to C-terminal 343 amino acids of
FT human plasma platelet-activating factor acetylhydrolase
FT (PAF-AH)"
XX
PN US6203790-B1.
XX
XX 20-MAR-2001.
PD
XX 23-MAY-2000; 2000US-00577758.
XX
PR 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
PR 07-JUN-1995; 95US-00480658.
PR 22-JAN-1998; 98US-00010715.
XX
PA (ICOS-) ICOS CORP.
XX
XX Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
PI Wilder CL;
XX
DR WPI; 2001-280610/29.
DR N-PSDB; AAD04168.
XX
XX Treating a mammal susceptible to or suffering from septicemia comprises
PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
PT supplement endogenous PAF-AH activity and to inactivate pathological
PT amounts of PAF.

XX Example 8; Col; 54pp; English.

XX The present sequence is mouse-human plasma platelet-activating factor

CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid

CC pRC/PH.MHC1. The invention relates to human plasma platelet-activating

CC factor acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The

CC invention also relates to method of treating a mammal susceptible to or

CC suffering from septicemia. PAF functions in normal physiological

CC processes such as inflammation, haemostasis and parturition. PAF-AH

CC specific antibodies are used in the diagnostic methods to detect abnormal

CC levels of PAF-AH in serum and also for treating the pathological

CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic

CC shock and arthritis. PAF-AH antibody is also useful for screening a

CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the

CC replacement of nucleotide G to T at position 996 within exon 9 resulting

CC in replacement of amino acid Val to Phe at position 279. Thus the

CC deficiency of PAF-AH activity is due to the genetic lesion in human

CC plasma PAF-AH gene. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 440 AA;

Query Match 99.6%; Score 908; DB 4; Length 440;

Best Local Similarity 99.4%; Pred. No. 7.4e-98;

Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

270 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 329

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

330 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 389

QY 121 FLQKHLGLHKDFDQWDCLEGGDDENLIPGTNINTTQNHIMLQNSSGIEKYN 171

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

390 FLQKHLGLHKDFDQWDCLEGGDDENLIPGTNINTTQNHIMLQNSSGIEKYN 440

RESULT 6

AAE00783

ID AAE00783 standard; protein; 440 AA.

XX AAE00783;

XX 11-SEP-2003 (revised)

DT 02-JUL-2001 (first entry)

XX

DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/PH.MHC2.

XX

XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;

KW antiinflammatory; septicemia; inflammation; haemostasis; parturition;

KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

XX

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX

Key Location/Qualifiers

FT Region 1..40

FT /note= "Corresponds to N-terminal 40 amino acids of mouse

FT plasma platelet-activating factor acetylhydrolase (PAF-

FT AH)"

FT 41..440

FT /note= "Corresponds to C-terminal 400 amino acids of

FT human plasma platelet-activating factor acetylhydrolase

FT (PAF-AH)"

XX

PN US6203790-B1.

XX

XX 20-MAR-2001.

XX

PF 23-MAY-2000; 2000US-00577758.

XX

PR 06-OCT-1993; 93US-00133803.

PR 06-OCT-1994; 94US-00318905.

PR 07-JUN-1995; 95US-00480658.

PR 22-JAN-1998; 98US-00010715.

XX (ICOS-) ICOS CORP.

XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;

PI Wilder CL;

XX WPI; 2001-280610/29.

DR N-PSDB; AAD04169.

XX

PT Treating a mammal susceptible to or suffering from septicemia comprises

PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to

PT supplement endogenous PAF-AH activity and to inactivate pathological

PT amounts of PAF.

XX

PS Example 8; Col; 54pp; English.

XX

CC The present sequence is mouse-human plasma platelet-activating factor

CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid

CC pRC/PH.MHC2. The invention relates to human plasma platelet-activating

CC factor acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The

CC invention also relates to method of treating a mammal susceptible to or

CC suffering from septicemia. PAF functions in normal physiological

CC processes such as inflammation, haemostasis and parturition. PAF-AH

CC specific antibodies are used in the diagnostic methods to detect abnormal

CC levels of PAF-AH in serum and also for treating the pathological

CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic

CC shock and arthritis. PAF-AH antibody is also useful for screening a

CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the

CC replacement of nucleotide G to T at position 996 within exon 9 resulting

CC in replacement of amino acid Val to Phe at position 279. Thus the

CC deficiency of PAF-AH activity is due to the genetic lesion in human

CC plasma PAF-AH gene. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 440 AA;

Query Match 99.6%; Score 908; DB 4; Length 440;

Best Local Similarity 99.4%; Pred. No. 7.4e-98;

Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

270 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 329

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

330 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 389

QY 121 FLQKHLGLHKDFDQWDCLEGGDDENLIPGTNINTTQNHIMLQNSSGIEKYN 171

Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

390 FLQKHLGLHKDFDQWDCLEGGDDENLIPGTNINTTQNHIMLQNSSGIEKYN 440

RESULT 7

AAR71913

ID AAR71913 standard; protein; 441 AA.

XX

AC AAR71913;

XX

DT 25-MAR-2003 (revised)

DT 05-DEC-1995 (first entry)

XX

DE Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).

XX

KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

KW disease; pleurisy; diagnosis.

XX

OS Homo sapiens.

XX

PN WO9509921-A1.
XX 13-APR-1995.
PD 06-OCT-1994; 94WO-US011340.
XX 06-OCT-1993; 93US-00133803.
PF 06-OCT-1993; 93US-00133803.
XX (ICOS-) ICOS CORP.
PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
XX WPI; 1995-155262/20.
DR N-PSDB; AAQ87947.
XX New nucleic acid encoding platelet activating factor, acetyl:hydrolase -
PT useful in diagnosis and for treating inflammatory diseases, e.g.
PT pleurisy.
XX Claim 5; Page 53-54; 88pp; English.
XX The human acetyl hydrolase gene (AAQ87947) has been isolated and
CC purified. The platelet activating factor acetyl hydrolase (AAR71913) is
CC useful in the treatment of inflammatory diseases, in particular pleurisy,
CC asthma, rhinitis and eczema. The gene may also be used in raising
CC monoclonal antibodies specific for PAF-AH that are useful in the
CC diagnosis of such diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 441 AA;
Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVIQTLSEDRFRGCIALDAWMPFLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFRGCIALDAWMPFLGDEVYSRIPQLFFINSEYFQYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKDIDSNAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKDIDSNAIDLNSKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 441
RESULT 8
AAR73046
ID AAR73046 standard; protein; 441 AA.
XX
AC AAR73046;
XX 25-MAR-2003 (revised)
DT 06-DEC-1995 (first entry)
XX Human acetyl hydrolase (AH) mutant C67S.
DE Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
KW Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 67
FT /note= "Wild-type Cys is substd. by Ser."
FT
XX WO9509921-A1.
PN 13-APR-1995.
XX 06-OCT-1994; 94WO-US011340.
PF 06-OCT-1994; 94WO-US011340.

XX 06-OCT-1993; 93US-00133803.
XX (ICOS-) ICOS CORP.
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
XX WPI; 1995-155262/20.
XX New nucleic acid encoding platelet activating factor, acetyl:hydrolase -
PT useful in diagnosis and for treating inflammatory diseases, e.g.
PT pleurisy.
XX Example 10; Page ?; 88pp; English.
XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying the
CC active site of AH. The sequences of these mutants are not given in the
CC patent specification; they have been derived from the original wild-type
CC protein (AAR71913). The AH gene and its product are useful in the
CC treatment of inflammatory diseases, in particular pleurisy, asthma,
CC rhinitis and eczema. The gene may also be used in raising monoclonal
CC antibodies specific for AH that are useful in the diagnosis of such
CC diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 441 AA;
Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVIQTLSEDRFRGCIALDAWMPFLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFRGCIALDAWMPFLGDEVYSRIPQLFFINSEYFQYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKDIDSNAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKDIDSNAIDLNSKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 441
RESULT 9
AAR73047
ID AAR73047 standard; protein; 441 AA.
XX
AC AAR73047;
XX 25-MAR-2003 (revised)
DT 06-DEC-1995 (first entry)
XX Human acetyl hydrolase (AH) mutant C229S.
DE Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
KW Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 229
FT /note= "Wild-type Cys is substd. by Ser."
FT
XX WO9509921-A1.
PN 13-APR-1995.
XX 06-OCT-1994; 94WO-US011340.
PF 06-OCT-1994; 94WO-US011340.
XX 06-OCT-1993; 93US-00133803.
PR 06-OCT-1993; 93US-00133803.

XX PA (ICOS-) ICOS CORP.
XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX DR WPI; 1995-155262/20.
XX XX New nucleic acid encoding platelet activating factor, acetyl:hydrolase -
PT useful in diagnosis and for treating inflammatory diseases, e.g.
PT pleurisy.
XX XX Example 10; Page ?; 88pp; English.
XX XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying the
CC active site of AH. The sequences of these muteins are not given in the
CC patent specification; they have been derived from the original wild-type
CC protein (AAR71913). The AH gene and its product are useful in the
CC treatment of inflammatory diseases, in particular pleurisy, asthma,
CC rhinitis and eczema. The gene may also be used in raising monoclonal
CC antibodies specific for AH that are useful in the diagnosis of such
CC diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX XX
SQ Sequence 441 AA;

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db |||||||
271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db |||||||
331 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db |||||||
391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 441

RESULT 10
AAR71920
ID AAR71920 standard; protein; 441 AA.
XX AC AAR71920;
XX XX 25-MAR-2003 (revised)
DT 06-DEC-1995 (first entry)
XX DE Human acetyl hydrolase (AH) mutant S108A.
XX XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
KW disease; pleurisy; diagnosis.
XX OS Homo sapiens.
XX XX Key Location/Qualifiers
FT Misc-difference 108 /note= "Wild-type Ser is substd. by Ala."
XX XX WO9509921-A1.
XX PN 13-APR-1995.
XX PD 06-OCT-1994; 94WO-US011340.
XX PF 06-OCT-1993; 93US-00133803.
XX PR (ICOS-) ICOS CORP.
XX PA

XX PI Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX DR WPI; 1995-155262/20.
XX XX New nucleic acid encoding platelet activating factor, acetyl:hydrolase -
PT useful in diagnosis and for treating inflammatory diseases, e.g.
PT pleurisy.
XX XX Example 10; Page ?; 88pp; English.
XX XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
CC purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
CC made with single amino acid changes for the purposes of identifying the
CC active site of AH. The sequences of these muteins are not given in the
CC patent specification; they have been derived from the original wild-type
CC protein (AAR71913). The AH gene and its product are useful in the
CC treatment of inflammatory diseases, in particular pleurisy, asthma,
CC rhinitis and eczema. The gene may also be used in raising monoclonal
CC antibodies specific for AH that are useful in the diagnosis of such
CC diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX XX
SQ Sequence 441 AA;

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db |||||||
271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db |||||||
331 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db |||||||
391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 441

RESULT 11
AAW23796
ID AAW23796 standard; protein; 441 AA.
XX AC AAW23796;
XX XX 25-MAR-2003 (revised)
DT 04-NOV-1997 (first entry)
XX DE Human plasma platelet activating factor acetylhydrolase.
XX XX Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;
KW pro-inflammatory arachidonic acid metabolite; reperfusion injury;
KW central nervous system shock; arthritis; Crohn's disease;
KW systemic lupus erythematosus; adult respiratory distress syndrome.
XX OS Homo sapiens.
XX XX US5641669-A.
XX XX 24-JUN-1997.
XX XX 06-OCT-1994; 94US-00318905.
XX XX 06-OCT-1993; 93US-00133803.
XX XX (ICOS-) ICOS CORP.
XX XX Tjoelker LW, Trong HL, Cousens LS, Wilder CL, Eberhardt CD;
XX PI Gray P;

DR WPI; 1997-340947/31.
DR N-PSDB; AAT80564.
XX
PT New human plasma platelet activating factor acetylhydrolase - useful as
PT anti-inflammatory for treatment of asthma, anaphylaxis, shock, etc.
XX
PS Claim 1; Col 35-38; 43pp; English.
XX
CC The present sequence represents the purified and isolated human plasma
CC platelet activating factor acetylhydrolase (PAF-AH). This novel
CC polypeptide inactivates PAF and oxidatively fragmented phospholipids such
CC as pro-inflammatory arachidonic acid metabolites, and so can be used to
CC treat inflammation by augmenting endogenous activity. Typical
CC applications are in asthma, anaphylaxis, shock, reperfusion injury,
CC central nervous system shock, arthritis, Crohn's disease, systemic lupus
CC erythematosus, adult respiratory distress syndrome. The polypeptide can
CC also be used to raise specific antibodies (Ab) which are useful as
CC immunoassay reagents and for generating anti-idiotypic antibodies. The
CC nucleic acid encoding the protein can be used to screen for related genes
CC ; in hybridisation assays to assess the protein- producing cells; to
CC generate knockout mice; to detect genetic mutations and (antisense
CC sequences) to inhibit the protein expression. Unlike PAF receptor
CC antagonists, the protein is a natural component of plasma. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX
SQ Sequence 441 AA;

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDOFRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
271 GHSFGGATVIQTLSEDOFRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 330

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNKAIDLSNKA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNKAIDLSNKA 390

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 441

RESULT 12
AAW09808
ID AAW09808 standard; protein; 441 AA.
XX
AC AAW09808;
XX
DT 25-MAR-2003 (revised)
DT 12-JUN-1997 (first entry)
XX
DE Platelet-activating factor acetylhydrolase.
XX
KW Human platelet-activating factor acetylhydrolase; PAF-AH; detection;
KW mutation; V279F; substitution; restriction fragment length polymorphism;
KW analysis; diagnosis; inherited; deficiency; severe respiratory symptom;
KW asthmatic children; treat; inflammatory condition.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .41
FT /label= signal peptide
FT /note= "possibly contains additional peptide that is
FT cleaved to yield the mature functional enzyme"
FT Protein 42. .441
FT /label= mature enzyme
FT Active-site 271. .275
FT /note= "contains active site serine; conforms to
FT consensus motif for mammalian and microbial lipases and
FT serine proteases"

XX US5605801-A.
PN
XX
PD 25-FEB-1997.
XX
PF 07-JUN-1995; 95US-00478465.
XX
PR 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
XX
PA (ICOS-) ICOS CORP.
XX
PI Gray P, Tjoelker LM, Trong HL, Cousens LS, Wilder CL;
PI Eberhardt CD;
XX
DR WPI; 1997-153573/14.
DR N-PSDB; AAT63701.
XX
PT Detection of platelet-activating factor acetylhydrolase gene mutation -
PT by restriction length polymorphism analysis.
XX
PS Example 3; Col 33-38; 43pp; English.
XX
CC This sequence is that of human platelet-activating factor acetyl-
CC hydrolase (PAF-AH). The claimed method of the invention detects a
CC mutation (which results in a V279F substitution) in the PAF-AH gene, and
CC comprises performing a restriction fragment length polymorphism analysis
CC and differentiating between wild-type and mutant alleles on the basis of
CC the number of restriction sites. The method is useful for diagnosis of
CC inherited PAF-AH deficiency, which has been correlated with severe
CC respiratory symptoms in asthmatic children. Recombinant PAF-AH can be
CC used to treat inflammatory conditions. (Updated on 25-MAR-2003 to correct
CC PF field.)
XX
SQ Sequence 441 AA;

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDOFRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
271 GHSFGGATVIQTLSEDOFRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 330

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNKAIDLSNKA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNKAIDLSNKA 390

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 441

RESULT 13
AAW26498
ID AAW26498 standard; protein; 441 AA.
XX
AC AAW26498;
XX
DT 25-MAR-2003 (revised)
DT 05-JAN-1998 (first entry)
XX
DE Human platelet-activating factor acetylhydrolase.
XX
KW Platelet-activating factor acetylhydrolase; PAF-AH; human; inflammation;
KW asthma; pleurisy; necrotising enterocolitis;
KW adult respiratory distress syndrome; therapy.
XX
OS Homo sapiens.
XX
PN US5656431-A.
PD 12-AUG-1997.

XX PF 07-JUN-1995; 95US-00483232.
XX PR 06-OCT-1993; 93US-00133803.
XX PR 06-OCT-1994; 94US-00318905.
XX PA (ICOS-) ICOS CORP.
XX PI Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;
XX PI Eberhardt CD;
XX DR WPI; 1997-414580/38.
XX DR N-PSDB; AAT87048.
XX PT Detecting lesions in human platelet-activating factor acetylhydrolase
XX PT gene - by comparison with defined wild-type gene sequence.
XX PS Example 3; Col 47-50; 53pp; English.
XX CC This polypeptide comprises human plasma platelet-activating factor
XX CC acetylhydrolase (PAF-AH), a protein that inactivates PAF and inactivates
XX CC oxidatively fragmented phospholipids such as products of the arachidonic
XX CC acid cascade that mediate inflammation. Its sequence was deduced from a
XX CC full-length cDNA clone (see AAT87048) obtained from a macrophage cDNA
XX CC library. Mouse, dog, cattle, chicken, rat and macaque PAF-AH polypeptides
XX CC (see AAW26500-505) have also been identified. Recombinant PAF-AH
XX CC polypeptides can be produced in prokaryotic or eukaryotic host cells and
XX CC used to mimic or augment normal processes of resolution of inflammation
XX CC in vivo. Examples describe the in vivo therapeutic effect of recombinant
XX CC PAF-AH products on acute inflammation, pleurisy, asthma, necrotizing
XX CC enterocolitis and adult respiratory distress syndrome in animal models.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 441 AA;
Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFOYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 441
RESULT 14
AAW38361
ID AAW38361 standard; protein; 441 AA.
XX AC AAW38361;
XX DT 31-MAR-1998 (first entry)
XX DE Human plasma platelet activating factor acetylhydrolase.
XX KW Human; plasma platelet activating factor acetylhydrolase;
XX KW monoclonal antibody; immunoassay; diagnosis; asthma; detection.
XX OS Homo sapiens.
XX PN US5698403-A.
XX PD 16-DEC-1997.
XX PF 07-JUN-1995; 95US-00483140.
XX

PR 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
XX (ICOS-) ICOS CORP.
XX PI Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;
XX PI Eberhardt CD;
XX DR WPI; 1998-051484/05.
XX DR N-PSDB; AAT96127.
XX PT Immunoassay for platelet activating factor acetylhydrolase, PAF-AH -
XX PT useful to diagnose disorders associated with abnormal PAF-AH level.
XX PS Claim 1; Col 35-38; 47pp; English.
XX CC The present sequence was used in the development of a method for
XX CC detecting human, mouse, canine, rat and monkey plasma platelet activating
XX CC factor acetylhydrolases (PAF-AH). The method comprises contacting serum
XX CC with PAF-AH specific monoclonal antibody (MAb) to form a PAF-AH/MAb
XX CC complex, and detecting the complex. The method can be used to diagnose
XX CC disorders associated with abnormal PAF-AH levels, and to monitor therapy
XX CC of such disorders. Plasma PAF-AH deficiency has been correlated with
XX CC severe respiratory symptoms in asthmatic children who appear to have
XX CC inherited the deficiency in an autosomal recessive manner
XX SQ Sequence 441 AA;
Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFOYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSSGIEKYN 441
RESULT 15
AAW96334
ID AAW96334 standard; protein; 441 AA.
XX AC AAW96334;
XX DT 28-JUN-1999 (first entry)
XX DE Human plasma platelet-activating factor acetylhydrolase (PAF-AH).
XX KW Plasma platelet activating factor acetylhydrolase; PAF-AH; PAF;
XX KW platelet activating factor; inflammation; treatment; hydrolysis;
XX KW augmentation; pleurisy; asthma; rhinitis; necrotizing enterocolitis;
XX KW acute respiratory distress syndrome; pancreatitis; neurological disease;
XX KW HIV; human immunodeficiency virus.
XX OS Homo sapiens.
XX PN WO9909147-A1.
XX PD 25-FEB-1999.
XX PF 13-AUG-1997; 97WO-US014212.
XX PR 13-AUG-1997; 97WO-US014212.
XX PA (ICOS-) ICOS CORP.
XX

PI Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
PI Wilder CL;

XX
DR WPI; 1999-181028/15.
DR N-PSDB; AAX08463.

XX
PT New truncated human platelet-activating factor acetylhydrolase and its
PT encoding polynucleotides - useful for regulating inflammatory events.

XX
PS Claim 1; Page 97-98; 136pp; English.

XX
CC Plasma platelet-activating factor acetylhydrolase (PAF-AH) can be used to
CC inactivate the pathological effects of PAF. Pathological conditions which
CC can be treated include pleurisy, asthma, rhinitis, necrotizing
CC enterocolitis, acute respiratory distress syndrome, acute pancreatitis or
CC neurological disease associated with HIV infection. Identification and
CC isolation of polynucleotide sequences encoding human plasma PAF-AH allows
CC the recombinant production of PAF-AH. This makes possible the use of
CC exogenous PAF-AH to mimic or augment normal processes of resolution of
CC inflammation in vivo. PAF inactivation occurs by hydrolysis of the PAF sn
CC -2 acetyl group by PAF-AH. PAF-AH also metabolises oxidatively fragmented
CC phospholipids such as products of the arachidonic acid cascade which
CC mediate inflammation. Administration of PAF-AH is advantageous to
CC administering PAF receptor antagonists since PAF-AH is a product normally
CC found in plasma. Because PAF receptor antagonists are structurally
CC related to PAF they competitively inhibit native PAF-AH activity.
CC Treatment with recombinant PAF-AH would augment endogenous PAF-AH
CC activity and compensate for any inactivated endogenous enzyme

XX
SQ Sequence 441 AA;

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSEDRFCGIALDAWMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
271 GHSFGGATVIQTLSEDRFCGIALDAWMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 330
Qy 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLKASLA 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLKASLA 390
Qy 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTNOHIMLQNSSGIEKYN 171
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
391 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTNOHIMLQNSSGIEKYN 441

Search completed: March 15, 2005, 10:03:44
Job time : 65.2647 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 09:57:26 ; Search time 17.0441 Seconds
(without alignments)
748.938 Million cell updates/sec

Title: US-09-922-067F-14_COPY_271_441
Perfect score: 912
Sequence: 1 GHSFGGATVIQTLSEDRFR.....INTTQHIMLQNSSGIEKYN 171

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	908	99.6	441	1 US-08-470-187-8	Sequence 8, Appli
2	908	99.6	441	1 US-08-318-905-8	Sequence 8, Appli
3	908	99.6	441	1 US-08-483-232-8	Sequence 8, Appli
4	908	99.6	441	1 US-08-483-140-8	Sequence 8, Appli
5	908	99.6	441	2 US-08-485-938A-8	Sequence 8, Appli
6	908	99.6	441	2 US-08-910-041-8	Sequence 8, Appli
7	908	99.6	441	3 US-09-328-474-8	Sequence 8, Appli
8	908	99.6	441	3 US-09-100-546-8	Sequence 8, Appli
9	908	99.6	441	3 US-09-010-715-8	Sequence 8, Appli
10	908	99.6	441	3 US-09-577-758-8	Sequence 8, Appli
11	776	85.1	444	2 US-08-485-938A-33	Sequence 33, Appl
12	749	82.1	444	1 US-08-483-140-28	Sequence 28, Appl
13	749	82.1	444	2 US-08-485-938A-32	Sequence 32, Appl
14	672	73.7	171	1 US-08-483-140-29	Sequence 29, Appl
15	672	73.7	171	2 US-08-485-938A-35	Sequence 35, Appl
16	592	64.9	440	1 US-08-483-140-27	Sequence 27, Appl
17	592	64.9	440	2 US-08-485-938A-31	Sequence 31, Appl
18	537.5	58.9	422	2 US-08-485-938A-34	Sequence 34, Appl
19	355	38.9	392	2 US-08-886-152-3	Sequence 3, Appli
20	355	38.9	392	3 US-09-196-222-3	Sequence 3, Appli
21	335	36.7	392	2 US-08-886-152-1	Sequence 1, Appli
22	335	36.7	392	3 US-09-196-222-1	Sequence 1, Appli
23	186	20.4	37	2 US-08-557-892-1	Sequence 1, Appli
24	186	20.4	37	2 US-08-387-858A-1	Sequence 1, Appli
25	186	20.4	37	3 US-09-294-384B-1	Sequence 1, Appli
26	186	20.4	37	3 US-08-717-079-1	Sequence 1, Appli
27	170	18.6	30	2 US-08-557-892-2	Sequence 2, Appli

28	170	18.6	30	2 US-08-387-858A-2	Sequence 2, Appli
29	170	18.6	30	3 US-09-294-384B-2	Sequence 2, Appli
30	170	18.6	30	3 US-08-717-079-2	Sequence 2, Appli
31	104	11.4	20	2 US-08-557-892-11	Sequence 11, Appl
32	104	11.4	20	2 US-08-387-858A-11	Sequence 11, Appl
33	104	11.4	20	3 US-09-294-384B-11	Sequence 11, Appl
34	104	11.4	20	3 US-08-717-079-11	Sequence 11, Appl
35	104	11.4	27	2 US-08-557-892-3	Sequence 3, Appli
36	104	11.4	27	2 US-08-387-858A-3	Sequence 3, Appli
37	104	11.4	27	3 US-09-294-384B-3	Sequence 3, Appli
38	104	11.4	27	3 US-08-717-079-3	Sequence 3, Appli
39	78	8.6	777	4 US-09-270-767-46717	Sequence 46717, A
40	77.5	8.5	321	4 US-09-543-681A-7186	Sequence 7186, Ap
41	77	8.4	460	4 US-09-248-796A-18517	Sequence 18517, A
42	75.5	8.3	435	4 US-09-949-016-7141	Sequence 7141, Ap
43	75.5	8.3	989	4 US-09-079-030-218	Sequence 218, App
44	75	8.2	317	4 US-09-634-238-383	Sequence 383, App
45	75	8.2	317	4 US-09-634-238-413	Sequence 413, App

ALIGNMENTS

RESULT 1
US-08-470-187-8
; Sequence 8, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-470-187-8
Query Match 99.6%; Score 908; DB 1; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;

Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVIQTLSEDRFCRGIALDAWMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAWMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNTTNOHIMLQNSGGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNTTNOHIMLQNSGGIEKYN 441

RESULT 2

US-08-318-905-8
; Sequence 8, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-905-8

Query Match 99.6%; Score 908; DB 1; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVIQTLSEDRFCRGIALDAWMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAWMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120

Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNTTNOHIMLQNSGGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNTTNOHIMLQNSGGIEKYN 441
RESULT 3
US-08-483-232-8
; Sequence 8, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5656431and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-232-8

Query Match 99.6%; Score 908; DB 1; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVIQTLSEDRFCRGIALDAWMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAWMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 390
QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNTTNOHIMLQNSGGIEKYN 171

Db 391 FLQKHLGLHKDFDQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 441

RESULT 4

US-08-483-140-8
; Sequence 8, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-140-8

Query Match 99.6%; Score 908; DB 1; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 330
Qy 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAIDLNSKASLA 390
Qy 121 FLQKHLGLHKDFDQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 441

RESULT 5

US-08-485-938A-8
; Sequence 8, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:

; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-8

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPANIIK 330
Qy 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAIDLNSKASLA 390
Qy 121 FLQKHLGLHKDFDQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 441

RESULT 6

US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai

APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,041
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-910-041-8

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPAIIK 60
Db 271 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPAIIK 330
Qy 61 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
Qy 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTQHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTQHIMLQNSSGIEKYN 441

RESULT 7
US-09-328-474-8
Sequence 8, Application US/09328474
Patent No. 6045794
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.

APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/328,474
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-328-474-8

Query Match 99.6%; Score 908; DB 3; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPAIIK 60
Db 271 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIPQLFFINSEYFQYPAIIK 330
Qy 61 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
Qy 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTQHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTQHIMLQNSSGIEKYN 441

RESULT 8
US-09-100-546-8
Sequence 8, Application US/09100546
Patent No. 6099836
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.

; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,758
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/010,715
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6203790and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-577-758-8

Query Match 99.6%; Score 908; DB 3; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 330

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKGDIDSNAAIDLSNKSALA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKGDIDSNVAIDLSNKSALA 390

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTNOHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTNOHIMLQNSSGIEKYN 441

RESULT 11
US-08-485-938A-33
; Sequence 33, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-33

Query Match 85.1%; Score 776; DB 2; Length 444;
Best Local Similarity 84.2%; Pred. No. 1.5e-86;
Matches 144; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 60
Db 272 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 331

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKGDIDSNAAIDLSNKSALA 120
Db 332 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKGDIDSNVAIDLSNKSALA 391

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTNOHIMLQNSSGIEKYN 171
Db 392 FLQKHLGLHKDFDQWDCLEGGDENLIPGNTNTTNOHIMLQNSTGIERPN 442

RESULT 12
US-08-483-140-28
; Sequence 28, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-140-28

Query Match      82.1%; Score 749; DB 1; Length 444;
Best Local Similarity 82.5%; Pred. No. 3.1e-83;
Matches 141; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFRGCIADAWMFLGDEVYSRIPQLFFINSEYFQYPAIIK 60
Db 272 GHSFGGATVLQALSEDRFRGCIADAWMLPLDDAIYSRIPQLFFINSEYFQYPAIIK 331

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFTGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db 332 MKKCYSPDKERKMITIRGSHQNFADFTFTGKIIGHMLKLKGDIDSNAAIDLSNKASLA 391

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTNQHIMLQNSSGIEKYN 171
Db 392 FLQKHLGLRKDFDQWDCLEGGDENLIPGTNINTNQHIMLQNSSGIEKYN 442

RESULT 13
US-08-485-938A-32
; Sequence 32, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
```

```
;
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-32

Query Match      82.1%; Score 749; DB 2; Length 444;
Best Local Similarity 82.5%; Pred. No. 3.1e-83;
Matches 141; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFRGCIADAWMFLGDEVYSRIPQLFFINSEYFQYPAIIK 60
Db 272 GHSFGGATVLQALSEDRFRGCIADAWMLPLDDAIYSRIPQLFFINSEYFQYPAIIK 331

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFTGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db 332 MKKCYSPDKERKMITIRGSHQNFADFTFTGKIIGHMLKLKGDIDSNAAIDLSNKASLA 391

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTNQHIMLQNSSGIEKYN 171
Db 392 FLQKHLGLRKDFDQWDCLEGGDENLIPGTNINTNQHIMLQNSSGIEKYN 442

RESULT 14
US-08-483-140-29
; Sequence 29, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
```

```
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-938A-35

Query Match          73.7%; Score 672; DB 2; Length 171;
Best Local Similarity 73.7%; Pred. No. 2.3e-74;
Matches 126; Conservative 14; Mismatches 31; Indels 0; Gaps 0

QY      1 GHSEGGATVQTLSSEDQRFCGIALDAMWFLGDDEVYSRIQPQLFFINSEYFQYPANIIK 60
         ||||| | | | | | | | | | | | | | : | | | | | | | | | | | | |
Db       1 GHSEGGATVFQALSEDQRFCGIALDPWMFPVSEELYSRVPQLPFFINSAEFTPKDI AK 60
         ||||| | | | | | | | | | | | | | : | | | | | | | | | | | | |

QY      61 MKKCYSPDKERKMITIRGSVHONFADETFATGKIIGHMLKLKGDDIDSNAAIDLNKA SLA 120
         || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       61 MNFYQPDKERKMITI KGSVHQNFADGTFTVGKIIGNKLSLKGDDIDSRVAIDL TNKASLA 120
         || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      121 FLQHLGLHKDFDQWDCLIEGD DENLI PGVTNTTNOHIMLNQSSGIEKY N 171
         || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       121 FLQHLGLHKDFDQWDCLVEGENENLIPGSPFDVVVTQSPALQSSPGSHNQ N 171
         || | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Search completed: March 15, 2005, 10:09:42
Job time : 18.0441 secs
```

```
;
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-140-29

Query Match      73.7%; Score 672; DB 1; Length 171;
Best Local Similarity 73.7%; Pred. No. 2.3e-74;
Matches 126; Conservative 14; Mismatches 31; Indels 0; Gaps 0

QY    1   GHSGGGATVIQTLSAQDQRFRRCGIALDAWMFPLGLDEWYSRIQPQLFFINSEFYQYPANIIK 60
      ||||| | | | | | | | | | | | | | : : : | | | | | | | | | | : | |
Db    1   GHSGGGATVFOALSEDQRFRCGIALDPWMFPVSEELYSRVLPQPLFFINSAEFTQPKDIK 60

QY    61  MKKCYSPDKERKMITIRGSVHQNFADFTTATGKIIGHMLKLKGIDISNAAILDNKASLA 120
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    61  MNFYQPDKERKMITIKGSVHQNFADGTFTVTGKIIGNKLSLKGIDISRVAIDLTKASLA 120

QY    121 FLQHLGLHKKDFDQWDCLEIGDDENLIPTNTINTNQHIMLNSSGIEKYN 171
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121 FLQHLGLHKKDFDQWDCLVGEENENLIPGSPFDVVVTQSPALQSPPGSHNQN 171
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
Run on: March 15, 2005, 10:07:52 ; Search time 51.1324 Seconds
(without alignments)
1103.088 Million cell updates/sec

Title: US-09-922-067F-14_COPY_271_441
Perfect score: 912
Sequence: 1 GHSFGGATVIQTLSEDRFR.....INTTQHIMLQNSSGIEKYN 171

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	912	100.0	441	16	US-10-741-601-373
2	912	100.0	441	16	US-10-741-601-374
3	908	99.6	441	9	US-09-729-402-8
4	908	99.6	441	14	US-10-003-978A-8
5	908	99.6	441	14	US-10-161-127-1
6	908	99.6	441	16	US-10-755-889-278
7	355	38.9	392	10	US-09-961-253-3
8	335	36.7	392	10	US-09-961-253-1
9	186	20.4	37	9	US-09-922-067-1
10	186	20.4	37	14	US-10-173-233-1
11	186	20.4	37	14	US-10-406-156-1
12	186	20.4	384	15	US-10-369-493-5034
13	184	20.2	476	15	US-10-369-493-6760
					Sequence 373, App
					Sequence 374, App
					Sequence 8, Appli
					Sequence 1, Appli
					Sequence 278, App
					Sequence 3, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 1, Appli
					Sequence 5034, Ap
					Sequence 6760, Ap

14	170	18.6	30	9	US-09-922-067-2	Sequence 2, Appli
15	170	18.6	30	14	US-10-173-233-2	Sequence 2, Appli
16	170	18.6	30	14	US-10-406-156-2	Sequence 2, Appli
17	133	14.6	438	15	US-10-369-493-2350	Sequence 2350, Ap
18	104	11.4	20	9	US-09-922-067-11	Sequence 11, Appl
19	104	11.4	20	14	US-10-173-233-11	Sequence 11, Appl
20	104	11.4	20	14	US-10-406-156-11	Sequence 11, Appl
21	104	11.4	27	9	US-09-922-067-3	Sequence 3, Appli
22	104	11.4	27	14	US-10-173-233-3	Sequence 3, Appli
23	104	11.4	27	14	US-10-406-156-3	Sequence 3, Appli
24	93.5	10.3	439	15	US-10-354-437-112	Sequence 112, App
25	82.5	9.0	401	14	US-10-156-761-8015	Sequence 8015, Ap
26	81.5	8.9	408	15	US-10-282-122A-52450	Sequence 52450, A
27	81	8.9	521	16	US-10-686-947-250	Sequence 250, App
28	81	8.9	521	16	US-10-686-947-270	Sequence 270, App
29	81	8.9	521	16	US-10-686-947-274	Sequence 274, App
30	77	8.4	460	15	US-10-425-114-47561	Sequence 47561, A
31	76.5	8.4	483	9	US-09-888-615-79	Sequence 79, Appl
32	76.5	8.4	483	14	US-10-131-985-53	Sequence 53, Appl
33	76.5	8.4	483	17	US-10-901-417-53	Sequence 53, Appl
34	76	8.3	502	15	US-10-282-122A-54571	Sequence 54571, A
35	75.5	8.3	194	15	US-10-425-114-42047	Sequence 42047, A
36	75	8.2	273	15	US-10-369-493-11644	Sequence 11644, A
37	75	8.2	273	15	US-10-369-493-15162	Sequence 15162, A
38	75	8.2	275	15	US-10-369-493-14679	Sequence 14679, A
39	75	8.2	317	9	US-09-971-536-44	Sequence 44, Appl
40	74.5	8.2	496	9	US-09-974-592-10	Sequence 10, Appl
41	74.5	8.2	496	9	US-09-201-936-10	Sequence 10, Appl
42	74.5	8.2	496	16	US-10-636-065-225	Sequence 225, App
43	74.5	8.2	496	16	US-10-600-272-10	Sequence 10, App
44	74	8.1	451	9	US-09-874-923-108	Sequence 108, App
45	74	8.1	451	9	US-09-991-496-108	Sequence 108, App

ALIGNMENTS

RESULT 1
US-10-741-601-373
; Sequence 373, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-373

Query Match 100.0%; Score 912; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.2e-93;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GHSFGGATVIQTLSEDRFRGCGIALDAWNFLGDEVYSRIPQPLFFINSEYFYQYPANIIK 60
Db	271	GHSFGGATVIQTLSEDRFRGCGIALDAWNFLGDEVYSRIPQPLFFINSEYFYQYPANIIK 330
Qy	61	MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLKGDIDSNAIDLNSKASLA 120
Db	331	MKKCYSPDKERKMITIRGSHQNFADFTATGKIIGHMLKLKGDIDSNAIDLNSKASLA 390
Qy	121	FLQKHLGLHKDFDQWDCLEGGDDENLIPGTNINTTQNHIMLQNSSGIEKYN 171
Db	391	FLQKHLGLHKDFDQWDCLEGGDDENLIPGTNINTTQNHIMLQNSSGIEKYN 441

RESULT 2
US-10-741-601-374
; Sequence 374, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-374

Query Match 100.0%; Score 912; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.2e-93;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330

Qy 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKDIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKDIDSNAAIDLSNKASLA 390

Qy 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSGGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSGGIEKYN 441

RESULT 3
US-09-729-402-8
; Sequence 8, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,402
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20010021379Aland, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-729-402-8

Query Match 99.6%; Score 908; DB 9; Length 441;
Best Local Similarity 99.4%; Pred. No. 2e-92;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330

Qy 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKDIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKDIDSNAAIDLSNKASLA 390

Qy 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSGGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNINTTNOHIMLQNSGGIEKYN 441

RESULT 4
US-10-003-978A-8
; Sequence 8, Application US/10003978A
; Publication No. US20030072747A1
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, Gerstein & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6357
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/003,978A
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/729,402
; FILING DATE: 04-DEC-2000
; APPLICATION NUMBER: US 09/577,758
; FILING DATE: 23-MAY-2000
; APPLICATION NUMBER: US 09/010,715
; FILING DATE: 22-JAN-1998
; APPLICATION NUMBER: US 08/480,658
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994

```

; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. US20030072747Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/37792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-003-978A-8

Query Match          99.6%; Score 908; DB 14; Length 441;
Best Local Similarity 99.4%; Pred. No. 2e-92;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANI 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANI 330

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 390

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNNTTNOHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNNTTNOHIMLQNSSGIEKYN 441

RESULT 5
US-10-161-127-1
; Sequence 1, Application US/10161127
; Publication No. US20030166225A1
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; TITLE OF INVENTION: ISOLATED GENOMIC POLYNUCLEOTIDE FRAGMENTS THAT ENCODE
; FILE REFERENCE: JR-16,001
; CURRENT APPLICATION NUMBER: US/10/161,127
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/294,404
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-127-1

Query Match          99.6%; Score 908; DB 14; Length 441;
Best Local Similarity 99.4%; Pred. No. 2e-92;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANI 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANI 330

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 390

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNNTTNOHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNNTTNOHIMLQNSSGIEKYN 441
```

```

RESULT 6
US-10-755-889-278
; Sequence 278, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-278

Query Match          99.6%; Score 908; DB 16; Length 441;
Best Local Similarity 99.4%; Pred. No. 2e-92;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANI 60
Db 271 GHSFGGATVIQTLSEDRFCRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPANI 330

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 390

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNNTTNOHIMLQNSSGIEKYN 171
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNNTTNOHIMLQNSSGIEKYN 441

RESULT 7
US-09-961-253-3
; Sequence 3, Application US/09961253
; Publication No. US20030040093A1
; GENERAL INFORMATION:
; APPLICANT: ADACHI, HIDEKI
; TSUJIMOTO, MASAFUMI
; ARAI, HIROYUKI
; INOUE, KEIZO
; TITLE OF INVENTION: PLATELET ACTIVATING FACTOR
; ACETYLHYDROLASE, AND GENE THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/961,253
; FILING DATE: 25-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,222
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,152
```

```

; FILING DATE: 30-JUN-1997
; APPLICATION NUMBER: JP 8-188369
; FILING DATE: 28-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2292-041-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-961-253-3

Query Match 38.9%; Score 355; DB 10; Length 392;
Best Local Similarity 45.7%; Pred. No. 9.2e-31;
Matches 69; Conservative 31; Mismatches 49; Indels 2; Gaps 1;

Qy 1 GHSFGGATVIQTLSEDRFRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPAIIK 60
Db 234 GHSFGGATAILALAKETQFRCAVALDAMFPLEDRDFYPKAGPVPFFINTEKFQTMESVNL 293
Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHML--KLKGDIDSNAAILDLSNKAS 118
Db 294 MKKICAQHQSRITVLGSHVRSQTDFAFTGNLIGKFFSTETRGSLDPYEGQVMVRAM 353
Qy 119 LAFLQKHLGLHKDFDQWDCLEGGDENLIPG 149
Db 354 LAFLQKHLGLKEDYQNNLNIEGIGPSLTPG 384

RESULT 8
US-09-961-253-1
; Sequence 1, Application US/09961253
; Publication No. US20030040093A1
; GENERAL INFORMATION:
; APPLICANT: ADACHI, HIDEKI
; TSUJIMOTO, MASAFUMI
; ARAI, HIROYUKI
; INOUE, KEIZO
; TITLE OF INVENTION: PLATELET ACTIVATING FACTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/961,253
; FILING DATE: 25-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,222
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,152
; FILING DATE: 30-JUN-1997

```

```

; APPLICATION NUMBER: JP 8-188369
; FILING DATE: 28-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2292-041-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: BOVINE (Bos taurus)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-961-253-1

Query Match 36.7%; Score 335; DB 10; Length 392;
Best Local Similarity 44.4%; Pred. No. 1.6e-28;
Matches 67; Conservative 23; Mismatches 59; Indels 2; Gaps 1;

Qy 1 GHSFGGATVIQTLSEDRFRGIALDAMFPLGDEVYSRIPQPLFFINSEYFQYPAIIK 60
Db 234 GHSFGGATAILALAKEMQFRCAVALDAMFPLEHDFTYPTARGPIFFINAEKFTQVETVNL 293
Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLK--LKGDIDSNAAILDLSNKAS 118
Db 294 MKKICDQHQSRITVLGSHVRSRLTDFVFNAGNWSKFFSSHTRGSLDPYEGQETVVVRAM 353
Qy 119 LAFLQKHLGLHKDFDQWDCLEGGDENLIPG 149
Db 354 LAFLQKHLGLKEDYQNNNFIEGIGPSLTPG 384

RESULT 9
US-09-922-067-1
; Sequence 1, Application US/09922067
; Patent No. US20020177209A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
; TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
; Thereof And Use Of The Same In Diagnosis And Therapy
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,067
; FILING DATE: 03-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/193,130
; FILING DATE: 1998-11-17
; APPLICATION NUMBER: PCT/GB94/01374

```



```
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; FEATURE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-406-156-1

Query Match      20.4%; Score 186; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 98 MLKLGKDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQ 134
    |||||
Db 1 MLKLGKDIDSNAAIDLSNKASLAFLQKHLGLHKDFDQ 37

RESULT 12
US-10-369-493-5034
; Sequence 5034, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5034
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5034

Query Match      20.4%; Score 186; DB 15; Length 384;
Best Local Similarity 32.5%; Pred. No. 6.6e-12;
Matches 40; Conservative 26; Mismatches 55; Indels 2; Gaps 1;

QY 1 GHSFGGATVIQTLSEDPFRGCIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIHK 60
    |||||
Db 234 GHSFGGATSIASSSD--FQKAIVLGWMYFLDQNOQEQAKQPIMLFLNVGDWQWNNLEV 291

QY 61 MKKCYSPDKERKMITIRGSHONFADFTATGKIIGHMLKLGKDIDSNAAIDLSNKASLA 120
    |||
Db 292 MRKILPNNEGNILLTSGAVHQSFDFPFPPNWLAKQFGVHGPTPEYLCMQSAIELTILS 351

QY 121 FLQ 123
    |||
Db 352 FLK 354

RESULT 13
US-10-369-493-6760
; Sequence 6760, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
```

```
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6760
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6760

Query Match      20.2%; Score 184; DB 15; Length 476;
Best Local Similarity 32.5%; Pred. No. 1.5e-11;
Matches 40; Conservative 24; Mismatches 59; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDPFRGCIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIHK 60
    |||||
Db 324 GHSFGGATSLASSAYTTDFQKAIVFDGWMYFLDSTQEQAKQPTLFLNVGDWQWNNLEVD 383

QY 61 MKKCYSPDKERKMITIRGSHONFADFTATGKIIGHMLKLGKDIDSNAAIDLSNKASLA 120
    |||
Db 384 MKKIISHNDGNLALTNGAVHQCFSDFFIFPSWLAKKFGVQGRTEPSLCMQAAIELSLA 443

QY 121 FLQ 123
    |||
Db 444 FLE 446

RESULT 14
US-09-922-067-2
; Sequence 2, Application US/09922067
; Patent No. US20020177209A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
; OF INVENTION: Thereof And Use Of The Same In Diagnosis And Therapy
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,067
; FILING DATE: 03-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/193,130
; FILING DATE: 1998-11-17
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
```


; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-922-067-2

Query Match 18.6%; Score 170; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 57
Db 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30

RESULT 15
US-10-173-233-2
; Sequence 2, Application US/10173233
; Publication No. US20030148398A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/173,233
; FILING DATE: 14-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,899
; FILING DATE: 12-May-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-173-233-2

Query Match 18.6%; Score 170; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 57

Db 1 WMFPLGDEVYSRIPQPLFFINSEYFQYPAN 30
Search completed: March 15, 2005, 10:25:10
Job time : 52.1324 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 09:56:51 ; Search time 14.25 Seconds
(without alignments)
1154.601 Million cell updates/sec

Title: US-09-922-067F-14_COPY_271_441
Perfect score: 912
Sequence: 1 GHSFGGATVIQTLSEDRFR.....INTTQHIMLQNSSGIEKYN 171

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	908	99.6	441	2 S60247	platelet-activatin
2	627.5	68.8	436	2 JC5021	platelet-activatin
3	186	20.4	384	2 T32756	hypothetical prote
4	184	20.2	476	2 T28936	hypothetical prote
5	133	14.6	438	2 T39268	hypothetical prote
6	129.5	14.2	450	2 G83740	hypothetical prote
7	84	9.2	317	2 D64220	methyltransferase
8	83	9.1	382	2 S56151	tubulin alpha chai
9	82.5	9.0	1154	2 A86318	protein F15H18.11
10	80	8.8	795	2 F82858	dipeptidyl-peptida
11	79.5	8.7	548	2 D90493	hypothetical prote
12	78	8.6	450	2 A45547	tubulin alpha-II c
13	78	8.6	1128	2 H90538	hypothetical prote
14	77.5	8.5	338	2 T23520	hypothetical prote
15	77.5	8.5	858	1 A42239	adenylate cyclase
16	77	8.4	828	2 G87584	hypothetical prote
17	76	8.3	391	2 T36311	probable lipase -
18	76	8.3	422	2 E69892	endo-xylanase homo
19	76	8.3	450	2 S31399	tubulin alpha chai
20	76	8.3	451	2 S04694	tubulin alpha chai
21	76	8.3	502	2 H81273	probable amino aci
22	76	8.3	603	2 T16298	hypothetical prote
23	75.5	8.3	162	2 D69439	conserved hypothet
24	75.5	8.3	989	2 I56333	apolipoprotein B -
25	75.5	8.3	1138	2 G71554	probable transmemb
26	75	8.2	275	2 B98301	non-heme chloroper
27	75	8.2	275	2 AF2982	non-heme chloroper
28	75	8.2	453	2 S16339	tubulin alpha chai
29	74.5	8.2	292	2 T33987	hypothetical prote

30	74.5	8.2	1347	2 T30909	endo-1,4-beta-xyla
31	74	8.1	214	2 AH3146	conserved hypothet
32	74	8.1	236	2 B98141	hypothetical prote
33	74	8.1	451	2 S33512	tubulin alpha chai
34	74	8.1	451	2 B53298	tubulin alpha-2 ch
35	74	8.1	1534	2 S59604	DNA (cytosine-5)-
36	74	8.1	1565	2 AD2135	polyketide synthas
37	73	8.0	188	2 E97251	spore protease GPR
38	73	8.0	381	2 S56148	tubulin alpha chai
39	73	8.0	453	2 S07459	tubulin alpha-I ch
40	73	8.0	534	2 H82244	sensor histidine k
41	73	8.0	649	1 W1WL6	E1 protein - human
42	72.5	7.9	286	2 D75217	probable 2-acetyl-
43	72.5	7.9	420	2 S27649	tabA protein - Pse
44	72.5	7.9	1096	1 S61917	protein kinase C (
45	72.5	7.9	1135	1 JQ1928	G2-G1 polyprotein

ALIGNMENTS

RESULT 1

S60247

platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C>Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C:Accession: S60247

R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf, B.; W.

Nature 374, 549-553, 1995

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase.

A:Reference number: S60247; MUID:95214779; PMID:7700381

A:Accession: S60247

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJO>

A:Cross-references: UNIPROT:Q13093; EMBL:U20157; NID:G780132; PIDN:AAC50126.1; PID:G7801

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 2.1e-80;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	GHSFGGATVIQTLSEDRFR	CGIALDAMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db	271	GHSFGGATVIQTLSEDRFR	CGIALDAMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
Qy	61	MKKCYSPDKERKMITIRG	SVHQNFADFTFATGKIIGHMLKLKGDIDSNAADLSNKASLA 120
Db	331	MKKCYSPDKERKMITIRG	SVHQNFADFTFATGKIIGHMLKLKGDIDSNAADLSNKASLA 390
Qy	121	FLQKHLGLHKDFDQWDC	LIEGDDENLIPGTNINTTNOHIMLQNSSGIEKYN 171
Db	391	FLQKHLGLHKDFDQWDC	LIEGDDENLIPGTNINTTNOHIMLQNSSGIEKYN 441

RESULT 2

JC5021

platelet-activating factor-acetylhydrolase (EC 3.1.1.-) precursor - guinea pig

N:Alternate names: PAF-acetylhydrolase

C:Species: Cavia porcellus (guinea pig)

C>Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

C:Accession: JC5021; PC4207

R:Karasawa, K.; Kuge, O.; Kawasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoyama, J. Biochem. 120, 838-844, 1996

A:Title: Cloning, expression and characterization of plasma platelet-activating factor-a

A:Reference number: JC5021; MUID:97103479; PMID:8947850

A:Accession: JC5021

A:Molecule type: DNA

A:Residues: 1-436 <KAR1>

A:Cross-references: UNIPROT:P70683; DDBJ:D67037; NID:g1644228; PIDN:BAA11054.1; PID:g164

A:Accession: PC4207

A:Molecule type: protein

A:Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392 <KAI

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83740
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <STO>
A;Cross-references: UNIPROT:Q9KEX2; GB:AP001509; GB:BA000004; NID:gl01731176; PIDN:BA044
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0727

Query Match 14.2%; Score 129.5; DB 2; Length 450;
Best Local Similarity 23.5%; Pred. No. 0.0001;
Matches 35; Conservative 28; Mismatches 49; Indels 37; Gaps 5;
QY 1 GHSFGGATVIQTLSEDRFRGCIADAWMFPLGDEVYSRIPQPLFFINS----- 49
Db 315 GHSFGGATTAQVMHQDPRIAGVNMDFLR--GSLIEGLDYPFMYMSGVVEVSMGPDG 372
QY 50 ---EYFQYPANIKMKKCYSPDKERK-----MITIRGSHVQNFADFTFATGKIIGH 97
Db 373 KKVEEAELPE---EFREFIADKKRKEGALKONGLYVVIENAEHESFSDWMLYSPLLDDR 429
QY 98 MLKLGKGDIDSNAAIDLSNKASLAFLOKHL 126
Db 430 DLPM-----LDQINKTLDDFFDEHL 449

RESULT 7
D64220
methytransferase ssoIM homolog - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: D64220
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
; C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: D64220
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-317 <TIGR>
A;Cross-references: UNIPROT:Q49400; GB:U39695; GB:L43967; NID:g1045833; PID:g1045868; TI
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
A;Start codon: GTG
C;Superfamily: site-specific methyltransferase EcoRI

Query Match 9.2%; Score 84; DB 2; Length 317;
Best Local Similarity 25.4%; Pred. No. 1.8;
Matches 30; Conservative 20; Mismatches 48; Indels 20; Gaps 4;
QY 48 NSEYFQY---PANIIKMKKCYSPDKERKMITIRGSHVQNFAD---FTFATGKIIGHMLKL 101
Db 47 NSHFFQFFQTFNQLQKK-----LIGFSFNLSQADKFTFDGNKVTXTKLG 94
QY 102 KGDIDSNAAIDLSNKASLAFLOKHLGKDFQDQWCLIEGDDENLIPGTNINTNQHI 159
Db 95 NGDFSDESIEVLKQADIVVTNPPFSLFQSF--IDLLIQHNKQFLVLGLNAAVSYNHI 150

RESULT 8
S56151
tubulin alpha chain - Spathidium sp. (fragment)
C;Species: Spathidium sp.
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: S56151
R;Tourancheau, A.B.; Tsao, N.; Klobutcher, L.A.; Pearlman, R.E.; Adoutte, A.

EMBO J. 14, 3262-3267, 1995
A;Title: Genetic code deviations in the ciliates: evidence for multiple and independent
A;Reference number: S56148; MUID:95347352; PMID:7621837
A;Accession: S56151
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-382 <TOU>
A;Cross-references: UNIPROT:Q27216; EMBL:Z49848; NID:g861141; PIDN:CAA90009.1; PID:g8611
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C;Superfamily: tubulin
C;Keywords: heterodimer; microtubule

Query Match 9.1%; Score 83; DB 2; Length 382;
Best Local Similarity 22.6%; Pred. No. 2.8;
Matches 40; Conservative 29; Mismatches 68; Indels 40; Gaps 9;
QY 7 ATVIQTLSEDRFRGCIADAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIIKMKKCYC 66
Db 202 AQVISSLTASLRFDGALNVDVTXFQTNLVPYPRI---HFMSSY---APIISAERAY- 252
QY 67 PDKERKMITIRGSHVQNFADFTFAT-----GKIIGHMLKLGDI---DSNAAI-DLSNK 116
Db 253 ---HEQLSVAEITNSSFEFASMAKCDPRHGKYMCCMMVRGDDVVPKDVVAAVATIKTK 308
QY 117 ASLAFLOKHLGKDFQW-----DCLIEGDDENLIPGTNINTNQHI-MLQNSSGI 167
Db 309 RTI-----QFDDWCPTGFKCGINYPPTTVVPGDLAKVMRAVCMISNSTAI 354

RESULT 9
A86318
protein F15H18.11 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86318
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86318
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1154 <STO>
A;Cross-references: UNIPROT:Q9LPQ6; GB:AE005172; NID:g6714300; PIDN:AAF25996.1; GSPDB:GN
C;Genetics:
A;Gene: F15H18.11
A;Map position: 1

Query Match 9.0%; Score 82.5; DB 2; Length 1154;
Best Local Similarity 26.3%; Pred. No. 13;
Matches 36; Conservative 22; Mismatches 60; Indels 19; Gaps 6;
QY 45 FFINSEYFQYPANIIKMKKCYSPDKERKMITIR---GSVHQNFAFT-----FATGKI 94
Db 6 FFISFVVF-----SVADLPSCFSADQQYEECRSRNLTCGSGHRVFESTTYPFWGGFNKPKF 61
QY 95 IGH-MLKLGKGDIDSNAAIDLSNKASLAFLOKHLGKDFQDQWCLIEGDDENLIPGTNIN 153
Db 62 CGHSSFKLSCGEGDQNLTLAIGN-ITLRVVSANLEHDKISVADDSLLDGGCLNI---WNFN 117
QY 154 TTNQHIMLQNSSGIEKY 170
Db 118 GKNQFTLDSNTETIDVF 134
RESULT 10

Search completed: March 15, 2005, 10:08:37
Job time : 15.25 secs

Query Match	8.5%	Score 77.5;	DB 1;	Length 858;
Best Local Similarity	21.2%;	Pred. No. 27;		
Matches 36;	Conservative 24;	Mismatches 75;	Indels 35;	Gaps 6;
QY	36	VYSRIPQPLFFINSEY-----FQYPANIIKMKCYSPDKERKMITRG-----S	79	
	:	:	:	:
DB	604	IYEFPPSGLOALNIENLNNTDAGCENCSKILKITYAYSQPDHSTSNYYHHGDDNSPPPPPS	663	

THIS PAGE BLANK (08709)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 09:48:35 ; Search time 63.7059 Seconds
(without alignments)
1374.528 Million cell updates/sec

Title: US-09-922-067F-14_COPY_271_441
Perfect score: 912
Sequence: 1 GHSFGGATVIQTLSEDRFR.....INTNQHIMLQNSSGIEKYN 171

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	908	99.6	441	1	PAFA_HUMAN
2	776	85.1	444	1	PAFA_BOVIN
3	749	82.1	444	1	PAFA_CANFA
4	634	69.5	440	2	Q921T4
5	633	69.4	440	2	Q8BKM3
6	627.5	68.8	436	1	PAFA_CAVPO
7	592	64.9	440	1	PAFA_MOUSE
8	537.5	58.9	422	1	PAFA_CHICK
9	535	58.7	404	2	Q6NYI7
10	355	38.9	392	1	PAF2_HUMAN
11	350	38.4	390	1	PAF2_RAT
12	338	37.1	390	1	PAF2_MOUSE
13	335	36.7	392	1	PAF2_BOVIN
14	308	33.8	362	2	Q6GPX8
15	304	33.3	346	2	Q9DB74
16	186	20.4	384	2	Q44753
17	184	20.2	388	1	PAFA_CAEEL
18	139	15.2	920	2	Q7SCR4
19	133	14.6	438	2	Q9URV1
20	129.5	14.2	450	2	Q9KEX2
21	105.5	11.6	609	2	Q7S2B3
22	104	11.4	468	2	Q81UC8
23	104	11.4	468	2	Q6HML0
24	102.5	11.2	402	2	Q70K06
25	97	10.6	378	2	Q65IY4
26	97	10.6	468	2	Q73CM7
27	96	10.5	468	2	Q81H53
28	94.5	10.4	386	2	Q9F2X9
29	92.5	10.1	509	2	Q8LSC7
30	90	9.9	456	2	Q81E25
31	89.5	9.8	3589	2	Q6LFF3

RESULT 1									
PAFA_HUMAN									
ID	PAFA_HUMAN	STANDARD;	PRT;	441	AA.				
AC	Q13093; Q15692; Q81VA2;								
DT	01-NOV-1997 (Rel. 35, Created)								
DT	01-NOV-2004 (Rel. 35, Last sequence update)								
DT	25-OCT-2004 (Rel. 45, Last annotation update)								
DE	Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)								
DE	(PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated								
DE	phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine								
DE	esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).								
GN	Name=PLA2G7; Synonyms=PAFAH;								
OS	Homo sapiens (Human)								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.								
RC	TISSUE=Myeloid;								
RX	MEDLINE=95214779; PubMed=7700381; DOI=10.1038/374549a0;								
RA	Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,								
RA	Schimpf B., Hooper S., le Trong H., Cousens L.S., Zimmerman G.A.,								
RA	Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;								
RT	"Anti-inflammatory properties of a platelet-activating factor								
RT	acetylhydrolase.";								
RL	Nature 374:549-553(1995).								
RN	[2]								
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.								
RC	TISSUE=Lymphoma;								
RX	MEDLINE=96197208; PubMed=8624782;								
RA	Tew D.G., Southan C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,								
RA	Moore K., Gloger I.S., Macphee C.H.;								
RT	"Purification, properties, sequencing, and cloning of a lipoprotein-								
RT	associated, serine-dependent phospholipase involved in the oxidative								
RT	modification of low-density lipoproteins.";								
RL	Arterioscler. Thromb. Vasc. Biol. 16:591-599(1996).								
RN	[3]								
RP	SEQUENCE FROM N.A., AND VARIANT ALA-379.								
RC	TISSUE=Blood;								
RX	MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;								
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,								
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,								
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,								
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,								
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,								
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,								
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,								
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,								
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,								
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,								
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,								
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,								
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,								
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,								

Q7njz2 gloeobacter
Q8s384 brassica ju
Q92m36 rhizobium m
Q8ms38 drosophila
Q8ehb8 shewanella
Q49400 mycoplasma
Q8qtb8 white spot
Q91l86 white spot
Q8vaq8 white spot
Q27216 spathidium
Q8rx30 arabidopsis
Q82qn6 streptomyce
Q9lpq6 arabidopsis
Q8px46 methanosarc

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP MUTAGENESIS.
 RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
 RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H., Zimmerman G.A.,
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad.";
 RL J. Biol. Chem. 270:25481-25487 (1995).
 RN [5]
 RP VARIANT PLA2G7 DEFICIENCY PHE-279.
 RX MEDLINE=96259525; PubMed=8675689;
 RA Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W., Eberhardt C.,
 RA Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A., McIntyre T.M.,
 RA Gray P.W., Prescott S.M.;
 RT "Platelet-activating factor acetylhydrolase deficiency. A missense
 RT mutation near the active site of an anti-inflammatory phospholipase.";
 RL J. Clin. Invest. 97:2784-2791 (1996).
 RN [6]
 RP VARIANT PLA2G7 DEFICIENCY ARG-281.
 RX MEDLINE=97396177; PubMed=9245731; DOI=10.1006/bbrc.1997.7047;
 RA Yamada Y., Yokota M.;
 RT "Loss of activity of plasma platelet-activating factor acetylhydrolase
 RT due to a novel Gln281-->Arg mutation.";
 RL Biochem. Biophys. Res. Commun. 236:772-775 (1997).
 RN [7]
 RP VARIANT PLA2G7 DEFICIENCY PHE-279.
 RX MEDLINE=98074100; PubMed=9412624;
 RA Hiramoto M., Yoshida H., Imaizumi T., Yoshimizu N., Satoh K.;
 RT "A mutation in plasma platelet-activating factor acetylhydrolase
 RT (Val279-->Phe) is a genetic risk factor for stroke.";
 RL Stroke 28:2417-2420 (1997).
 RN [8]
 RP VARIANT PLA2G7 DEFICIENCY PHE-279.
 RX MEDLINE=98132308; PubMed=9472966;
 RA Yamada Y., Ichiara S., Fujimura T., Yokota M.;
 RT "Identification of the G994-->T missense in exon 9 of the plasma
 RT platelet-activating factor acetylhydrolase gene as an independent risk
 RT factor for coronary artery disease in Japanese men.";
 RL Metabolism 47:177-181 (1998).
 RN [9]
 RP VARIANT PLA2G7 DEFICIENCY PHE-279.
 RX MEDLINE=98430412; PubMed=9759612;
 RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,
 RA Yoshimizu N., Fukushi K., Satoh K.;
 RT "A mutation in plasma platelet-activating factor acetylhydrolase
 RT (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not
 RT for hypertension.";
 RL Thromb. Haemost. 80:372-375 (1998).
 RN [10]
 RP VARIANTS HIS-92; THR-198 AND ALA-379.
 RX MEDLINE=20311534; PubMed=10733466;
 RA Kruse S., Mao X.-Q., Heinzmann A., Blattmann S., Roberts M.H.,
 RA Braun S., Gao P.-S., Forster J., Kuehr J., Hopkin J.M., Shirakawa T.,
 RA Deichmann K.A.;
 RT "The Ile198Thr and Ala379Val variants of plasmatic PAF-acetylhydrolase
 RT impair catalytical activities and are associated with atopy and
 RT asthma.";
 RL Am. J. Hum. Genet. 66:1522-1530 (2000).
 CC -!- FUNCTION: Modulates the action of platelet-activating factor (PAF)
 CC by hydrolyzing the sn-2 ester bond to yield the biologically
 CC inactive lyso-PAF. Has a specificity for substrates with a short
 CC residue at the sn-2 position. It is inactive against long-chain
 CC phospholipids.
 CC -!- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
 CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: Plasma.

CC -!- POLYMORPHISM: The alleles Thr-198 and Val-379 are associated with
 CC atopy and asthma.
 CC -!- DISEASE: Defects in PLA2G7 are the cause of platelet-activating
 CC factor acetylhydrolase deficiency (PLA2G7 deficiency)
 CC [MIM:601690]. It is a trait which is present in 27% of Japanese.
 CC It could have a significant physiologic effect in the presence of
 CC inflammatory bodily responses.
 CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
 CC family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U20157; AAC50126.1; -.
 CC EMBL; U24577; AAB04170.1; -.
 CC EMBL; BC038452; AAH38452.1; -.
 CC PIR; S60247; S60247.
 CC Genew; HGNC:9040; PLA2G7.
 CC MIM; 601690; -.
 CC GO; GO:0005576; C:extracellular; TAS.
 CC GO; GO:0005543; F:phospholipid binding; TAS.
 CC GO; GO:0006954; P:inflammatory response; TAS.
 CC GO; GO:0006629; P:lipid metabolism; TAS.
 CC InterPro; IPR008262; Lipase_AS.
 CC InterPro; IPR005065; PAF_Ac_hydrolase_II.
 CC InterPro; IPR000379; Ser_estrs.
 CC Pfam; PF03403; PAF-AH_p_II; 1.
 CC PROSITE; PS00120; LIPASE_SER; 1.
 CC KW Direct protein sequencing; Disease mutation; Glycoprotein; Hydrolase;
 KW Lipid degradation; Polymorphism; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 441 Platelet-activating factor
 FT acetylhydrolase.
 FT ACT_SITE 273 273 Charge relay system.
 FT ACT_SITE 296 296 Charge relay system.
 FT ACT_SITE 351 351 Charge relay system.
 FT CARBOHYD 423 423 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 433 433 N-linked (GlcNAc...)
 FT VARIANT 92 92 R -> H (common polymorphism;
 FT dbSNP:1805017).
 FT /FTID=VAR_011583.
 FT I -> T (common polymorphism;
 FT dbSNP:1805018).
 FT /FTID=VAR_011584.
 FT V -> F (in PLA2G7 deficiency; loss of
 FT function; more common among Japanese than
 FT in Caucasians; risk factor for coronary
 FT artery disease and stroke).
 FT /FTID=VAR_004268.
 FT Q -> R (in PLA2G7 deficiency; loss of
 FT function).
 FT /FTID=VAR_011585.
 FT V -> A (common polymorphism;
 FT dbSNP:1051931).
 FT /FTID=VAR_011586.
 FT S -> A: Activity is higher than wild type.
 FT S -> A: Loss of activity.
 FT D -> A: Almost no activity.
 FT D -> N: Diminished activity.
 FT D -> A: Loss of activity.
 FT D -> N: Loss of activity.
 FT D -> A: No change in activity.
 FT D -> A: Activity is higher than wild type.
 FT H -> A: Loss of activity.
 SQ SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;
 Query Match 99.6%; Score 908; DB 1; Length 441;
 Best Local Similarity 99.4%; Pred. No. 1.7e-79;

Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFRGCIADAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 60
|||||
Db 271 GHSFGGATVIQTLSEDRFRGCIADAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 330
|||||

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
|||||
Db 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 390
|||||

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNTTNOHIMLQNSGGIEKYN 171
|||||
Db 391 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNTTNOHIMLQNSGGIEKYN 441
|||||

RESULT 2
PAPA BOVIN
ID PAPA BOVIN STANDARD; PRT; 444 AA.
AC Q28017;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated
DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
DE esterase) (1-alkyl-2-acetyl-1-alkylglycerophosphocholine esterase).
GN Name=PLA2G7;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
RA McIntyre T.M., Staforini D.M., Prescott S.M., Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad";
RL J. Biol. Chem. 270:25481-25487(1995).
CC -!- FUNCTION: Modulates the action of platelet-activating factor (PAF)
CC by hydrolyzing the sn-2 ester bond to yield the biologically
CC inactive lyso-PAF. Has a specificity for substrates with a short
CC residue at the sn-2 position. It is inactive against long-chain
CC phospholipids.
CC -!- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U34247; AAC48483.1; -.
CC InterPro; IPR008262; Lipase AS.
CC InterPro; IPR005065; PAF_AC_hydrolase II.
CC InterPro; IPR000379; Ser_estra.
CC Pfam; PF03403; PAF-AH_p_II; 1.
CC PROSITE; PS00120; LIPASE_SER; 1.
KW Glycoprotein; Hydrolase; Lipid degradation; Signal.
FT SIGNAL 1 21 By similarity.
FT CHAIN 22 444 Platelet-activating factor
FT acetylhydrolase.
FT ACT_SITE 274 274 Charge relay system (By similarity).
FT ACT_SITE 297 297 Charge relay system (By similarity).

FT ACT_SITE 352 352 Charge relay system (By similarity).
FT CARBOHYD 60 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 200 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 424 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 434 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 444 AA; 50133 MW; 97689917BE2F4C38 CRC64;

Query Match 85.1%; Score 776; DB 1; Length 444;
Best Local Similarity 84.2%; Pred. No. 1.1e-66;
Matches 144; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFRGCIADAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 60
|||||
Db 272 GHSFGGATVIQTLSEDRFRGCIADAWMFPLGDEVYSRIPQPLFFINSEYFQYPANIIK 331
|||||

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
|||||
Db 332 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLKGDIDSNVAIDLSNKASLA 391
|||||

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNTTNOHIMLQNSGGIEKYN 171
|||||
Db 392 FLQKHLGLHKDFDQWDCLEGGDENLIPGTNTTNOHIMLQNSGGIEKYN 442
|||||

RESULT 3
PAPA CANFA
ID PAPA CANFA STANDARD; PRT; 444 AA.
AC Q28262;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated
DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
DE esterase) (1-alkyl-2-acetyl-1-alkylglycerophosphocholine esterase).
GN Name=PLA2G7;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
RA McIntyre T.M., Staforini D.M., Prescott S.M., Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad";
RL J. Biol. Chem. 270:25481-25487(1995).
CC -!- FUNCTION: Modulates the action of platelet-activating factor (PAF)
CC by hydrolyzing the sn-2 ester bond to yield the biologically
CC inactive lyso-PAF. Has a specificity for substrates with a short
CC residue at the sn-2 position. It is inactive against long-chain
CC phospholipids.
CC -!- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U34246; AAC48484.1; -.
CC InterPro; IPR008262; Lipase AS.
CC InterPro; IPR005065; PAF_AC_hydrolase II.
CC InterPro; IPR000379; Ser_estra.


```
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK051454; BAC34647.1; -.
DR MGD; MGI:1351327; Pla2g7.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006954; P:inflammatory response; TAS.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR005065; PAF_Ac_hydrolase II.
DR InterPro; IPR000379; Ser_estra.
DR Pfam; PF03403; PAF-AH_p_II; 1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 440 AA; 49258 MW; 17C8B4D28F1ADC94 CRC64;

Query Match 69.4%; Score 633; DB 2; Length 440;
Best Local Similarity 70.2%; Pred. No. 8e-53;
Matches 120; Conservative 17; Mismatches 34; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIQPQLFFINSEYFQYPANIIK 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
270 GHSFGGATVIQALSEDRFCRGVALDPMVYPVNEELYSRTIQLLLFINSKFPQTPKDIK 329

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAIDLNSKASLA 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
330 MKKFYQPKERKMITIKGSHVQNFDDFTFTGKIIGNKLTGKEIDSRVAIDLNTKASMA 389

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTINTNTNQHIMLQNSSGIEKYN 171
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
390 FLQKHLGLKQDFDQWDLPLVEGDDENLIPGSPFDAVTQVPAQHSQSGTQN 440

RESULT 6
PAFA_CAVPO STANDARD; PRT; 436 AA.
AC P70683;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
DE (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated
DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
DE esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).
GN Name=PLA2G7; Synonyms=PAFAH;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Liver;
RX MEDLINE=97103479; PubMed=8947850;
RA Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,
RA Yokoyama K., Setaka M., Nojima S.;
RT "Cloning, expression and characterization of plasma platelet-
activating factor-acetylhydrolase from guinea pig.";
RL J. Biochem. 120:838-844(1996).
CC -|- FUNCTION: Modulates the action of platelet-activating factor (PAF)
by hydrolyzing the sn-2 ester bond to yield the biologically
inactive lyso-PAF. Has a specificity for substrates with a short
residue at the sn-2 position. It is inactive against long-chain
phospholipids.
CC -|- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
CC -|- SUBCELLULAR LOCATION: Extracellular.
CC -|- TISSUE SPECIFICITY: Plasma.
CC -|- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D67037; BAA11054.1; -.
DR PIR; JC5021; JC5021.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR005065; PAF_Ac_hydrolase II.
DR InterPro; IPR000379; Ser_estra.
DR Pfam; PF03403; PAF-AH_p_II; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Glycoprotein; Hydrolase; Lipid degradation; Signal.
FT SIGNAL 1 21 By similarity.
FT CHAIN 22 436 Platelet-activating factor
acetylhydrolase.
FT ACT_SITE 271 271 Charge relay system (By similarity).
FT ACT_SITE 294 294 Charge relay system (By similarity).
FT ACT_SITE 349 349 Charge relay system (By similarity).
FT CARBOHYD 76 76 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 324 324 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 436 AA; 49062 MW; C359D96E392FFE11 CRC64;

Query Match 68.8%; Score 627.5; DB 1; Length 436;
Best Local Similarity 70.8%; Pred. No. 2.7e-52;
Matches 121; Conservative 19; Mismatches 26; Indels 5; Gaps 1;

QY 1 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIQPQLFFINSEYFQYPANIIK 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
269 GHSFGGATVIQTLSEDRFCGIALDPMFPVGVGDVHVKIPQLFFINSEYFQSANDTKK 328

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAIDLNSKASLA 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
329 IEKFYQPKERKMIAVKGSHVHNFVDFTFATGKIIGQMLSLKGLKIDSEVAMDINKASLA 388

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLIPGTINTNTNQHIMLQNSSGIEKYN 171
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
389 FLQKHLGLKQDFDQWDLPLVEGDDENLIPETIPTT-----MQSSTGTQQRN 434

RESULT 7
PAFA_MOUSE
ID PAFA_MOUSE STANDARD; PRT; 440 AA.
AC Q60963;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
```


Db 324 KMVKLSSNDTNKRMITIKGSHVHQSFPDFTFVSGBEIGKFFKLKGEIDPNEAIDICNHSAL 383

QY 120 AFLQKHLGLHKDFDQWDCLEIGDDENLIPGTNTIN 153

Db 384 AFLQKHLGLHKDFDQWDCLEIGDDENLIPGTNTIN 153

Db 384 AFLQKHLGLHKDFDQWDCLEIGDDENLIPGTNTIN 153

RESULT 9

Q6NYI7

ID Q6NYI7 PRELIMINARY; PRT; 404 AA.

AC Q6NYI7

DT 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)

DE Zgc:77563.

GN ORFNames=zgc:77563;

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Strausberg R.L.

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC066578; AAH66578.1; -.

DR ZFIN; ZDB-GENE-040426-2248; zgc:77563.

DR GO; GO:0008247; C:2-acetyl-1-alkylglycerophosphocholine ester. . . ; IEA.

DR GO; GO:0003847; F:1-alkyl-2-acetyl-1-alkylglycerophosphocholine ester. . . ; IEA.

DR GO; GO:0003824; F:catalytic activity; IEA.

DR GO; GO:0016042; P:lipid catabolism; IEA.

DR InterPro; IPR008262; Lipase AS.

DR InterPro; IPR005065; PAF_Ac_hydrolase II.

DR InterPro; IPR000379; Ser esters.

DR Pfam; PF03403; PAF-AH_p II; 1.

DR PROSITE; PS00120; LIPASE_SER; UNKNOWN 1.

SQ SEQUENCE 404 AA; 45743 MW; 2A2CEBEFCE0828F CRC64;

Query Match 58.7%; Score 535; DB 2; Length 404;

Best Local Similarity 62.3%; Pred. NO. 2.3e-43;

Matches 99; Conservative 27; Mismatches 33; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAWMFPLGDEVYSRIPOLFFINSEYFQYPAIIK 60

Db 246 GHSFGGATVIECLCKEVRFCGVALDTWMPDLDEIFPGVKQPIFFINSEKFWIGNIIR 305

QY 61 MKKCYSPDKERKMITIRGSHVHONFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120

Db 306 MKKLDSEAFPRKMITIKGTVHQSFPDFTFTGNWIGRLMKLKGIDPHIALDLCKATLA 365

QY 121 FLQKHLGLHKDFDQWDCLEIGDDENLIPGTNTINQHI 159

Db 366 FLQKHLGLHKDFDQWDCLEIGDDENLIPGTNTINQHI 159

Db 366 FLQKHLGLHKDFDQWDCLEIGDDENLIPGTNTINQHI 159

RESULT 10

PAF2 HUMAN

ID PAF2 HUMAN STANDARD; PRT; 392 AA.

AC Q99487; O15458;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Platelet-activating factor acetylhydrolase 2, cytoplasmic

DE (EC 3.1.1.47) (Serine dependent phospholipase A2) (HSD-PLA2).

GN Name=PAFAH2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=97115847; PubMed=8955149; DOI=10.1074/jbc.271.51.33032;

RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,

RA Aoki J., Hattori M., Arai H., Inoue K.;

RT "cDNA cloning and expression of intracellular platelet-activating

RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF

RT acetylhydrolase.";

RL J. Biol. Chem. 271:33032-33038 (1996).

RN [2]

RP SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.

RC TISSUE=Prostate;

RX MEDLINE=98161812; PubMed=9494101;

RA Rice S.Q.J., Southan C., Boyd H.F., Terrett J.A., Macphee C.H.,

RA Moores K., Gloger I.S., Tew D.G.;

RT "Expression, purification and characterization of a human serine-

RT dependent phospholipase A2 with high specificity for oxidized

RT phospholipids and platelet activating factor.";

RL Biochem. J. 330:1309-1315 (1998).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Eye;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [4]

RP REVIEW.

RX MEDLINE=97364701; PubMed=9218411; DOI=10.1074/jbc.272.29.17895;

RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;

RT "Platelet-activating factor acetylhydrolases.";

RL J. Biol. Chem. 272:17895-17898 (1997).

CC -!- FUNCTION: Has a marked selectivity for phospholipids with short

THIS PAGE BLANK (USPTO)